

Fig. 1

5'	9	18	27	36	45	54
GTG GGC ATG GTG GGC AAC GTC CTC CTG	63	72	81	90	99	108
--- --- --- --- --- ---	---	---	---	---	---	---
Val Gly Met Val Gly Asn Val Leu Leu Val	---	---	---	---	---	---
Leu His Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu	---	---	---	---	---	---
ATG TGC ACC GCC TGC GTG CCG CTC ACG CTC GGC AAC CTC GGC TTC GAC GTG GTC	---	---	---	---	---	---
Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly	---	---	---	---	---	---
TGG GTG TTC GGC GGC GGC CTC TGC CAC CAC CTG GTC TTC TTC CTG CAG CCG GTC ACC	---	---	---	---	---	---
Trp Val Phe Phe Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr	---	---	---	---	---	---
GTC TAT GTG TCG GTG TTC ACG CTC ACC ACC ATC GCA GTG GAC CCG TAC GTC GTG	---	---	---	---	---	---
Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr Val Val	---	---	---	---	---	---
CTG GTG CAC CCG CTC AGG CCG CGC ATC 3'	---	---	---	---	---	---
Leu Val His Pro Leu Arg Arg Arg Ile	---	---	---	---	---	---

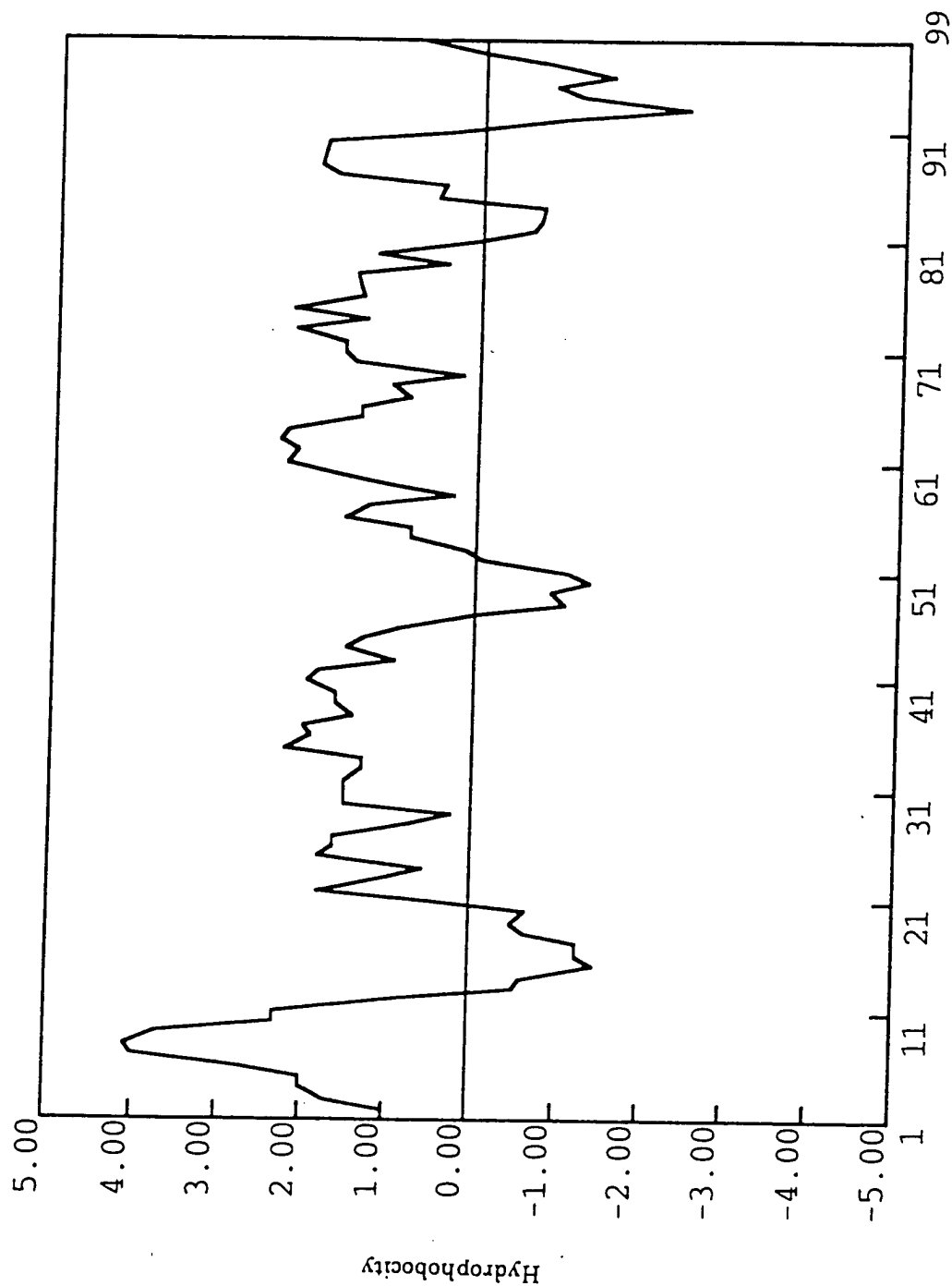
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Fig. 2

5'	GGC	CTG	CTG	CTG	GTC	ACC	TAC	CTG	CCT	CTG	CTG	ATC	CTC	CTG	TCT	TAC	54
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Gly	Leu	Leu	Leu	Val	Thr	Tyr	Leu	Leu	Pro	Leu	Val	Ile	Leu	Leu	Ser	Tyr
	63	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	GTC	CGG	GTG	TCA	GTG	AAG	CTC	CGC	CGC	GTG	GTG	CCG	GGC	TGC	GTG	ACC	108
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Val	Arg	Val	Ser	Val	Lys	Leu	Arg	Asn	Arg	Val	Pro	Gly	Cys	Val	Thr	Gln
	117	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	AGC	CAG	GCC	GAC	TGG	GAC	CGC	GCT	CGG	CGC	CGG	ACC	TTC	TGC	TTC	CTG	162
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Ser	Gln	Ala	Asp	Trp	Asp	Arg	Ala	Arg	Arg	Arg	Thr	Phe	Cys	Leu	Leu	Val
	171	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	GTG	GTC	GTG	GTG	GTC	TTT	GCC	ATC	TGC	TGG	TTC	CCT	TAC	TAC	3'		
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Val	Val	Val	Val	Val	Phe	Ala	Ile	Cys	Trp	Leu	Pro	Tyr	Tyr			

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Fig. 3



Position of amino acid on amino acid sequence

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Fig. 4

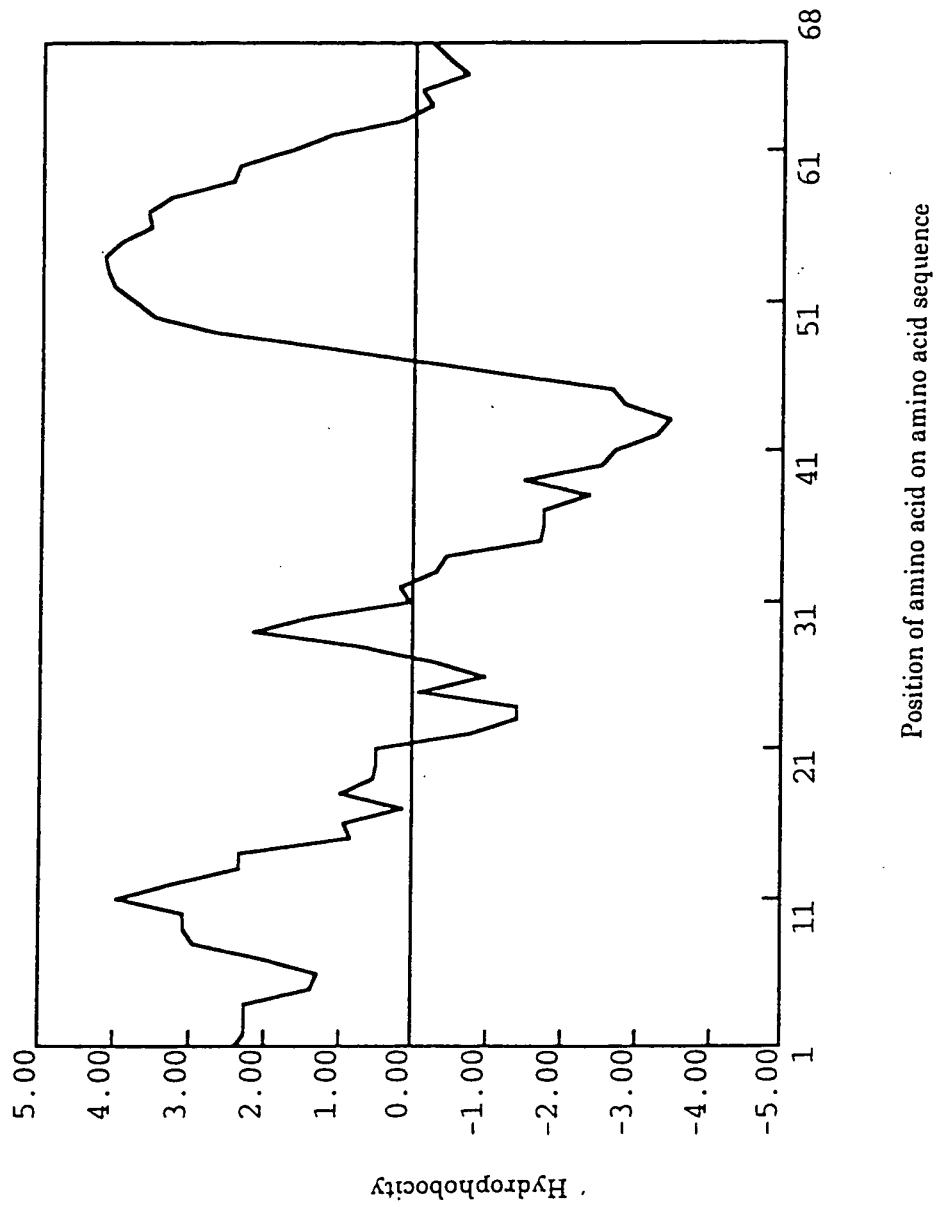


Fig. 5

p19P2	10	20	30	40	50
S12863	1 VGMVGNVLV	LVIAVRRLH	NVTNFLICNL	ALSDVLMCTA	CVPLTLAYAF
	1 LGVSGNIALI	IIILKQKEMR	NVTNILLVNL	SFSDLLAVVM	CLPFTFVYIL
p19P2	60	70	80	90	100
S12863	51 EPRGWFVFCGG	LCHLVFELQP	MTVYVSVETPL	TTIAVDRLVV	LVHPLRRRI-
	51 MDH-WVFEGET	MCKLNPEVQC	VSITVSIESL	VLIAVERHQL	IINPRGWRPN
p19P2	110	120	130	140	150
S12863	101 -----	-----	-----	-----	-----
	101 NRHAYIGITV	IWVLAVASSL	PFVIYQILTD	EPFQNVSLAA	FKDKYVCFDK
p19P2	160	170	180	190	200
S12863	151 -----GLLV	TYLLPLLVIL	LS-----	VRVSVKLRNR	VVPGCVTQSQ
	151 FPSDSHRLSY	ITLLLVQLQYF	GPLCFIFICY	FKIYIRLKR	NNMMDKIRDS
p19P2	210	220	230	240	250
S12863	201 ADWDRARRRR	TFCLLVVVVW	VFAICWLPFY	-----	-----
	201 KYRSSETKRI	NVMLLSIWA	-FAVCWLPPLT	-----	-----

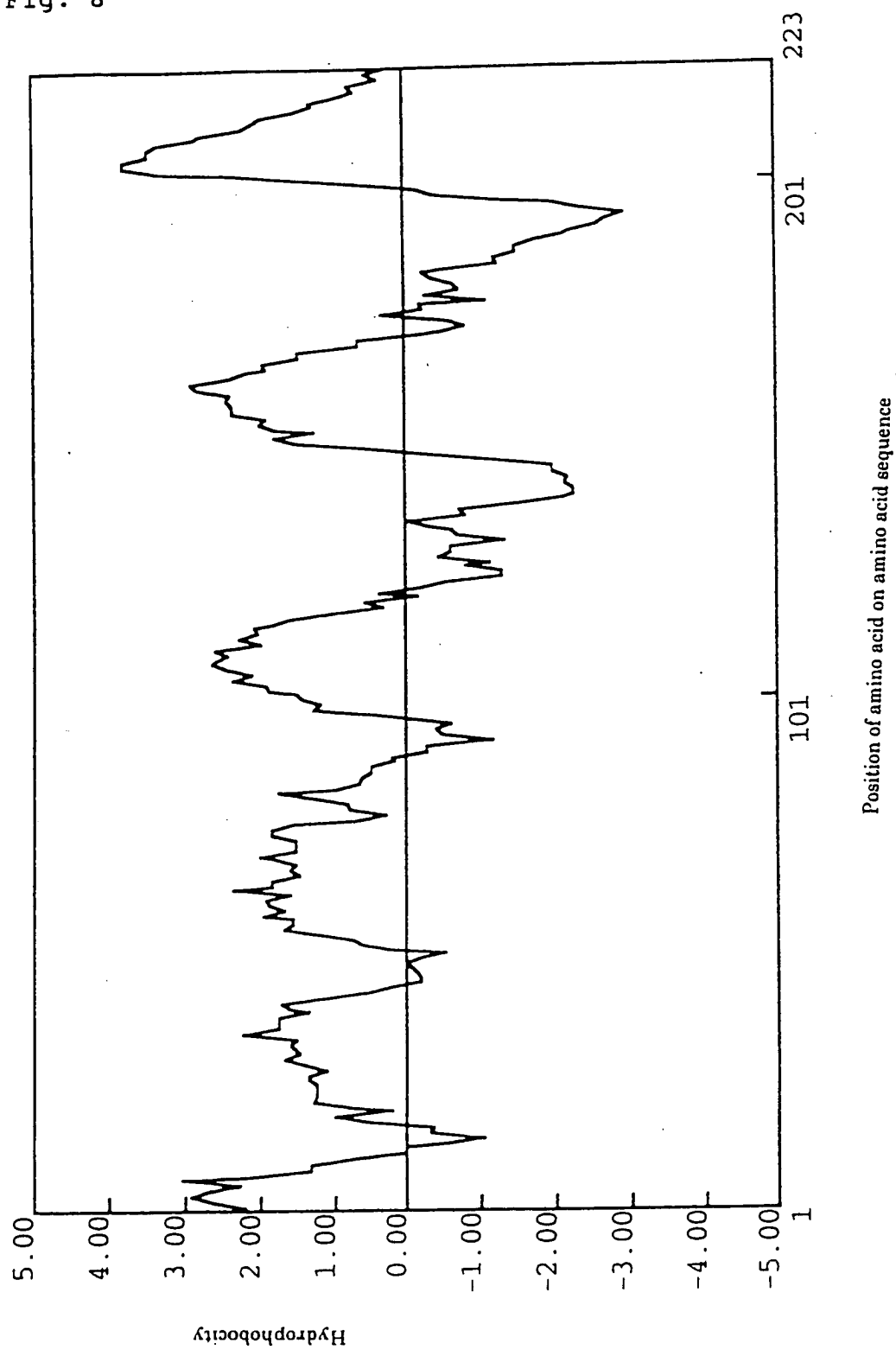
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Fig. 7

p19p2	1	10	20	30	40	50	50
pg3-2/pg1-10	1	VGAVGNVLLV	LVIARVRRH	NVTNFLIGNL	ALSDVLMCTA	CVPLTLAYAF	50
	1	VGAVGNVLLV	LVIARVRRLY	NVTNFLIGNL	ALSDVLMCTA	CVPLTLAYAF	50
p19p2	51	60	70	80	90	100	100
pg3-2/pg1-10	51	EPRG/VFGGG	LCHLVFFLQP	VTVYVSFTL	TTIAVDRYVV	LVHPLRRRI	100
	51	EPRG/VFGGG	LCHLVFFLQA	VTVYVSFTL	TTIAVDRYVV	LVHPLRRRI	100
p19p2	101	110	120	130	140	150	150
pg3-2/pg1-10	101	LRLSAYAVLA	IWVLSAVLAL	PAAVHTYHVE	LKPHDVRICE	EFWGSQERQR	150
p19p2	151	160	170	180	190	200	200
pg3-2/pg1-10	151	GLLLV	TYLLPLLVL	LSYVRVSVKL	RNRVVFECVT	QSQADVDRAR	200
	151	QLYAWGLLLV	TYLLPLLVL	LSYVRVSVKL	RNRVVFECVT	QSQADVDRAR	200
p19p2	201	210	220	230	240	250	250
pg3-2/pg1-10	201	RRRTFCLLV	VAVVFAI CML	PYY.....	250
	201	RRRTFCLLV	VAVVFTL CML	PFF.....	250

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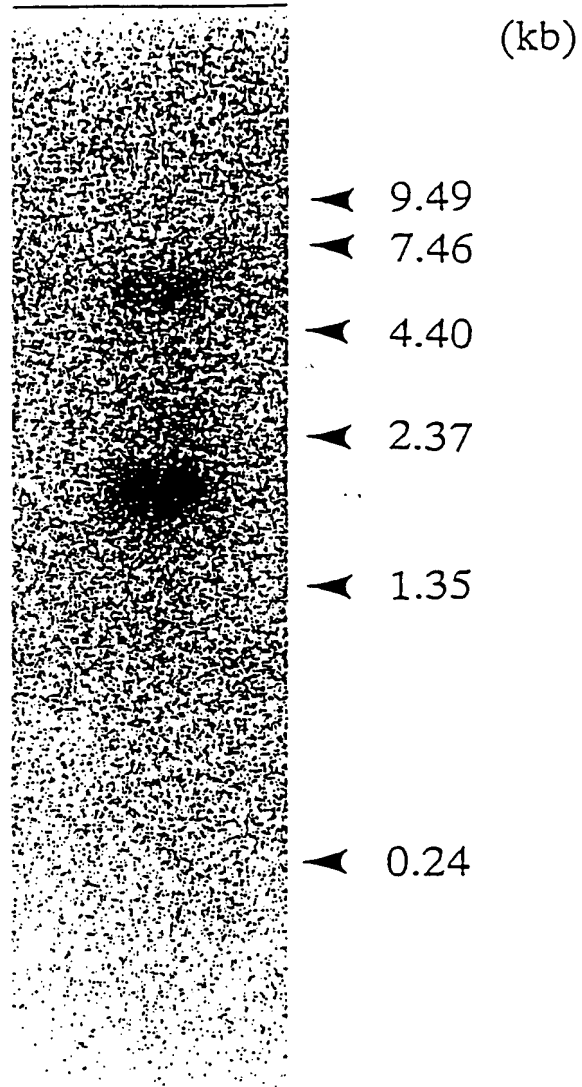
Fig. 8



1	CATCGTCAAGCAGATGAAGATCATCCACGAGGATGGCTACTCCGAGGCCAGCAGAAATT	60
1		1
61	CTGCCCCCTCTTCCCCGCGAGTGCTTTCCCCGCTCTCCAAACCCCACTCCCAGGTGGCCATG	120
1	Met	1
121	GCCTCATCGACCACCTCGGGGCCCCAGGGTTTCTGACTTATTTTCTGGGCTGCCGCCGGCG	180
2	AlaSerSerThrThrArgGlyProArgValSerAspLeuPheSerGlyLeuProProAla	21
181	GTCACAACCTCCCGCCAACCAGAGCGCAGAGGCCTCGGCGGGCAACGGGTCCGTGGCTGGC	240
22	ValThrThrProAlaAsnGlnSerAlaGluAlaSerAlaGlyAsnGlySerValAlaGly	41
241	GCGGACGCTCCAGCCGTCACGCCCTTCCAGAGCCTGCAGCTGGTGCATCAGCTGAAGGGG	300
42	AlaAspAlaProAlaValThrProPheGlnSerLeuGlnLeuValHisGlnLeuLysGly	61
301	CTGATCGTGCTGCTCTACAGCGTCGTGGTGGTGGTGGGGCTGGTGGGCAACTGCCTGCTG	360
62	LeuIleValLeuLeuTyrSerValValValValValGlyLeuValGlyAsnCysLeuLeu	81
361	GTGCTGGTGATCGCGCGGGTGGCGCGGCTGCACAACGTGACGAACCTTCCTCATCGGCAAC	420
92	ValLeuValIleAlaArgValArgArgLeuHisAsnValThrAsnPheLeuIleGlyAsn	101
421	CTGGCCTTGTCGACGTGCTCATGTGCACCGCCTGCGTGCCGCTCACGCTGGCCTATGCC	480
102	LeuAlaLeuSerAspValLeuMetCysThrAlaCysValProLeuThrLeuAlaTyrAla	121
481	TTGAGCCACGCGGCTGGGTGTTCGGCGGCGGCTGTGCCACCTGGTCTTCTTCCTGCAG	540
122	PheGluProArgGlyTrpValPheGlyGlyGlyLeuCysHisLeuValPhePheLeuGln	141
541	CCGGTCAACGCTCTATGTGTGGTGTTCACGCTCAACACCATCGCAGTGGACCGCTACGTC	600
142	ProValThrValTyrValSerValPheThrLeuThrThrIleAlaValAspArgTyrVal	161
501	GTGCTGGTGCACCCGCTGAGGCGGCGCATCTCGCTGCGCCTCAGCGCCTACGCTGTGCTG	660
162	ValLeuValHisProLeuArgArgArgIleSerLeuArgLeuSerAlaTyrAlaValLeu	181
561	GCCATCTGGGCGCTGTCCGCGGTGTGCGGCTGCCCGCCGCGCTGCACACCTATCACGTG	720
182	AlaIleTrpAlaLeuSerAlaValLeuAlaLeuProAlaAlaValHisThrTyrHisVal	201
721	GAGCTCAAGCCGCACGACGTGCGCCTCTGCGAGGAGTTCTGGGGCTCCAGGAGCGCCAG	780
202	GluLeuLysProHisAspValArgLeuCysGluGluPheTrpGlySerGlnGluArgGln	221
781	CGCCAGCTCTACGCCTGGGGGCTGCTGTGCTGGTCACTACCTGCTCCCTCTGCTGGTCATC	840
222	ArgGlnLeuTyrAlaTrpGlyLeuLeuLeuValThrTyrLeuLeuProLeuLeuValIle	241
841	CTCCTGTCTTACGTCCGGGTGTCACTGAAGCTCCGCAACCGGTGGTGCCGGGCTGCGTG	900
242	LeuLeuSerTyrValArgValSerValLysLeuArgAsnArgValValProGlyCysVal	261
901	ACCCAGAGCCAGGCCGACTGGGACCGCGCTCGGCGCCGCGCACCTTCTGCTTGCTGGTG	960
262	ThrGlnSerGlnAlaAspTrpAspArgAlaArgArgArgThrPheCysLeuLeuVal	281
961	GTGGTCTGTTGGTGGTGTTCGCCGCTCTGCTGGCTGCCGCTGCACGTCTTCAACCTGTGCGG	1020
282	ValValValValValPheAlaValCysTrpLeuProLeuHisValPheAsnLeuLeuArg	301
1021	GACCTCGACCCCCACGCCATCGACCCCTTACGCCTTTGGGCTGGTGCAGCTGCTCTGCCAC	1080
302	AspLeuAspProHisAlaIleAspProTyrAlaPheGlyLeuValGlnLeuLeuCysHis	321
1081	TGGCTCGCCATGAGTTCCGCGCTGCTACAACCCCTTCATCTACGCCTGGCTGCACGACAGC	1140
322	TrpLeuAlaMetSerSerAlaCysTyrAsnProPheIleTyrAlaTrpLeuHisAspSer	341
1141	TTCCGCGAGGAGCTGCGCAAACTGTGGTTCGCTTGGCCCCGCAAGATAGCCCCCATGGC	1200
342	PheArgGluGluLeuArgLysLeuLeuValAlaTrpProArgLysIleAlaProHisGly	361
1201	CAGAATATGACCGTCAGCGTGGTTCATCTGATGCCACTTAGCCAGGCCTTGGTCAAGGAGC	1260
362	GlnAsnMetThrValSerValValIle***	371
1261	TCCACTTCAACTGGCCTCCTAGGGCACCACTCGAGGTCAATCTGGTGTCTATTCTCAGCA	1320
		371
1321	CCAGAGCTAGC	1331
		371

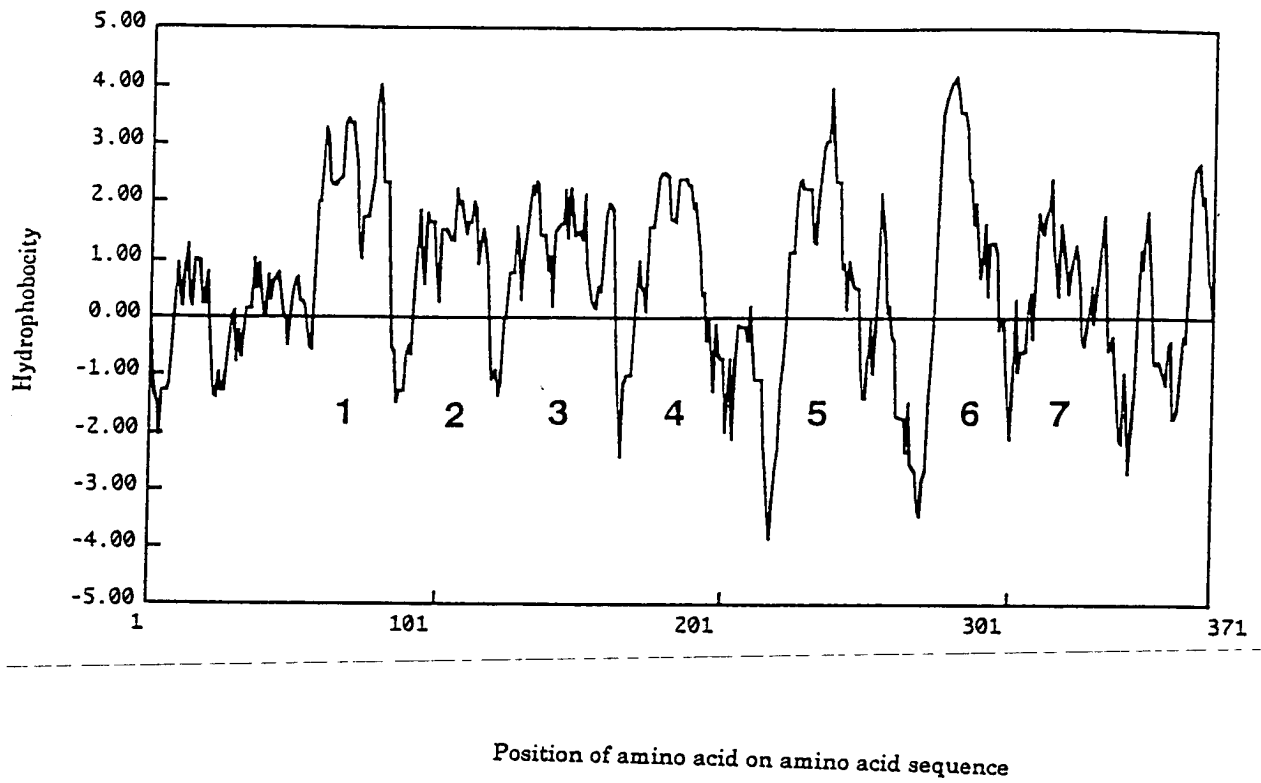
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Fig. 10



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Fig. 11



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Fig. 12

5'	CTG	TGT	GTC	ATC	GCG	GTG	GAT	AGG	TAC	GTG	GTT	CTG	GTG	CAC	CCG	CTA	CGT	CGG	
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Leu	Cys	Val	Ile	Ala	Val	Asp	Arg	Tyr	Val	Val	Leu	Val	His	Pro	Leu	Arg	Arg	
	CGC	ATT	TCA	CTG	AGG	CTC	AGC	GCC	TAC	GCG	GTG	CTG	GGC	ATC	TGG	GCT	CTA	TCT	
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Arg	Ile	Ser	Leu	Arg	Leu	Ser	Ala	Tyr	Ala	Val	Leu	Gly	Ile	Trp	Ala	Leu	Ser	
	GCA	GTG	CTG	GCG	CTG	CCG	GCC	GCG	GTG	CAC	ACC	TAC	CAT	GTG	GAG	CTC	AAG	CCC	
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ala	Val	Leu	Ala	Leu	Pro	Ala	Ala	Val	His	Thr	Tyr	His	Val	Glu	Leu	Lys	Pro	
	CAC	GAC	GTG	AGC	CTC	TGC	GAG	GAG	TTC	TGG	GGC	TCG	CAG	GAG	CGC	CAA	CGC	CAG	
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	His	Asp	Val	Ser	Leu	Cys	Glu	Glu	Phe	Trp	Gly	Ser	Gln	Glu	Arg	Gln	Arg	Gln	
	ATC	TAC	GCC	TGG	GGG	CTG	CTT	CTG	GGC	ACC	TAT	TTG	CTC	CCC	CTG	CTG	GCC	ATC	
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ile	Tyr	Ala	Trp	Gly	Leu	Leu	Leu	Gly	Thr	Tyr	Leu	Leu	Pro	Leu	Leu	Ala	Ile	
	CTC	CTG	TCT	TAC	GTA	CGG	GTG	TCA	GTG	AAG	CTG	AGG	AAC	CGC	GTG	GTG	CCT	GGC	
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Leu	Leu	Ser	Tyr	Val	Arg	Val	Ser	Val	Lys	Leu	Arg	Asn	Arg	Val	Val	Pro	Gly	
	AGC	GTG	ACC	CAG	AGT	CAA	GCT	GAC	TGG	GAC	CGA	GCG	CGT	CGC	CGC	CGC	ACT	TTC	
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ser	Val	Thr	Gln	Ser	Gln	Ala	Asp	Trp	Asp	Arg	Ala	Arg	Arg	Arg	Arg	Thr	Phe	
	TGT	CTG	CTG	GTG	GTG	GTG	GTG	GTA	GTG	TTC	ACG	CTC	TGC	TGG	CTG	CCC	TTC	TAC	
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Cys	Leu	Leu	Val	Val	Val	Val	Val	Val	Phe	Thr	Leu	Cys	Trp	Leu	Pro	Phe	Tyr	

CT 3'

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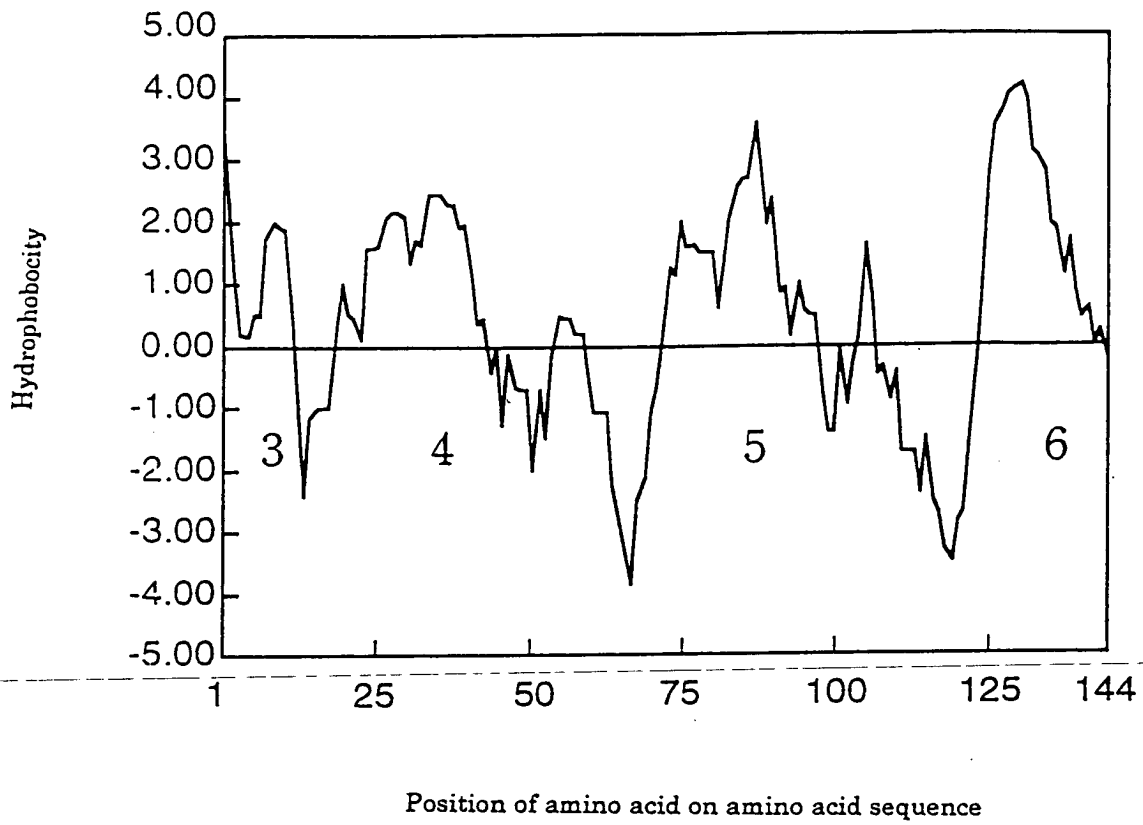
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Fig. 13

p19P2	1	10	20	30	40	50	50
pG3-2/pG1-10	1	1	1	1	1	1	1
p5S38	-79						-30
p19P2	51	60	70	80	90	100	100
pG3-2/pG1-10	51	51	51	51	51	51	51
p5S38	-29						21
p19P2	101	110	120	130	140	150	150
pG3-2/pG1-10	101	101	101	101	101	101	101
p5S38	22						71
p19P2	151	160	170	180	190	200	200
pG3-2/pG1-10	151	151	151	151	151	151	151
p5S38	72						121
p19P2	201	210	220	230	240	250	250
pG3-2/pG1-10	201	201	201	201	201	201	201
p5S38	122						171

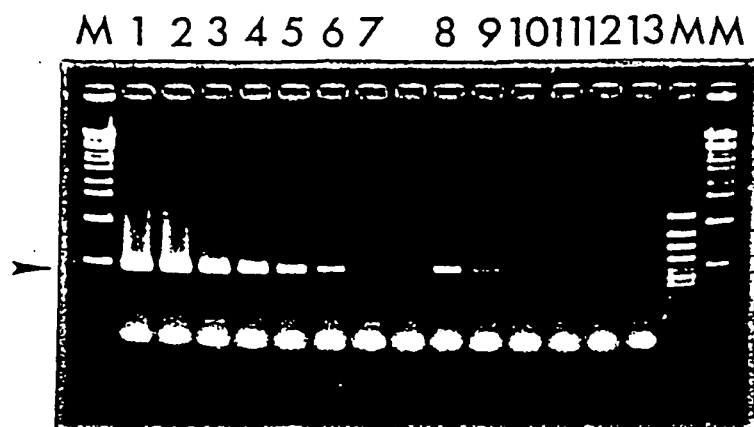
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Fig. 14



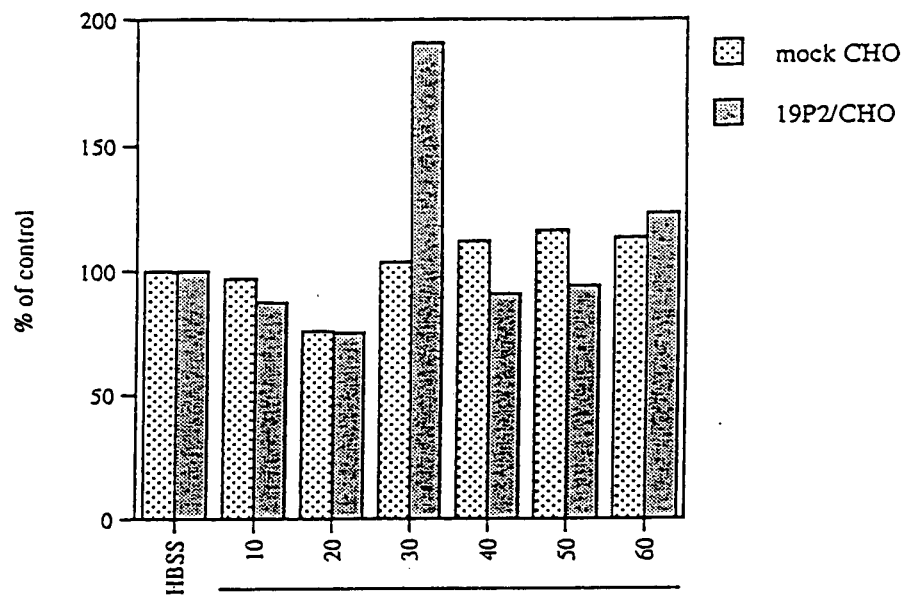
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Fig. 15



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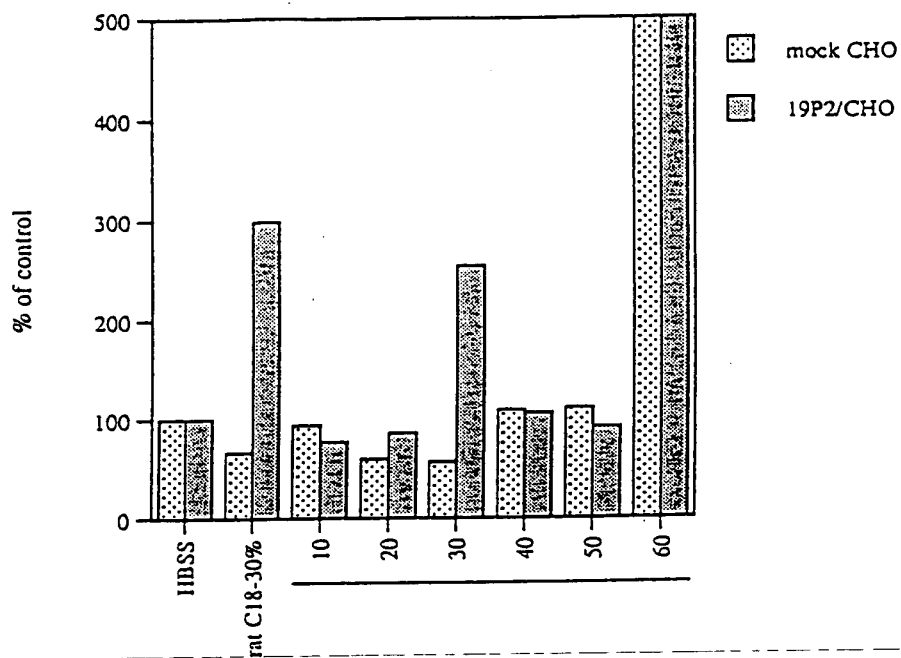
Fig. 16



66032-1539100

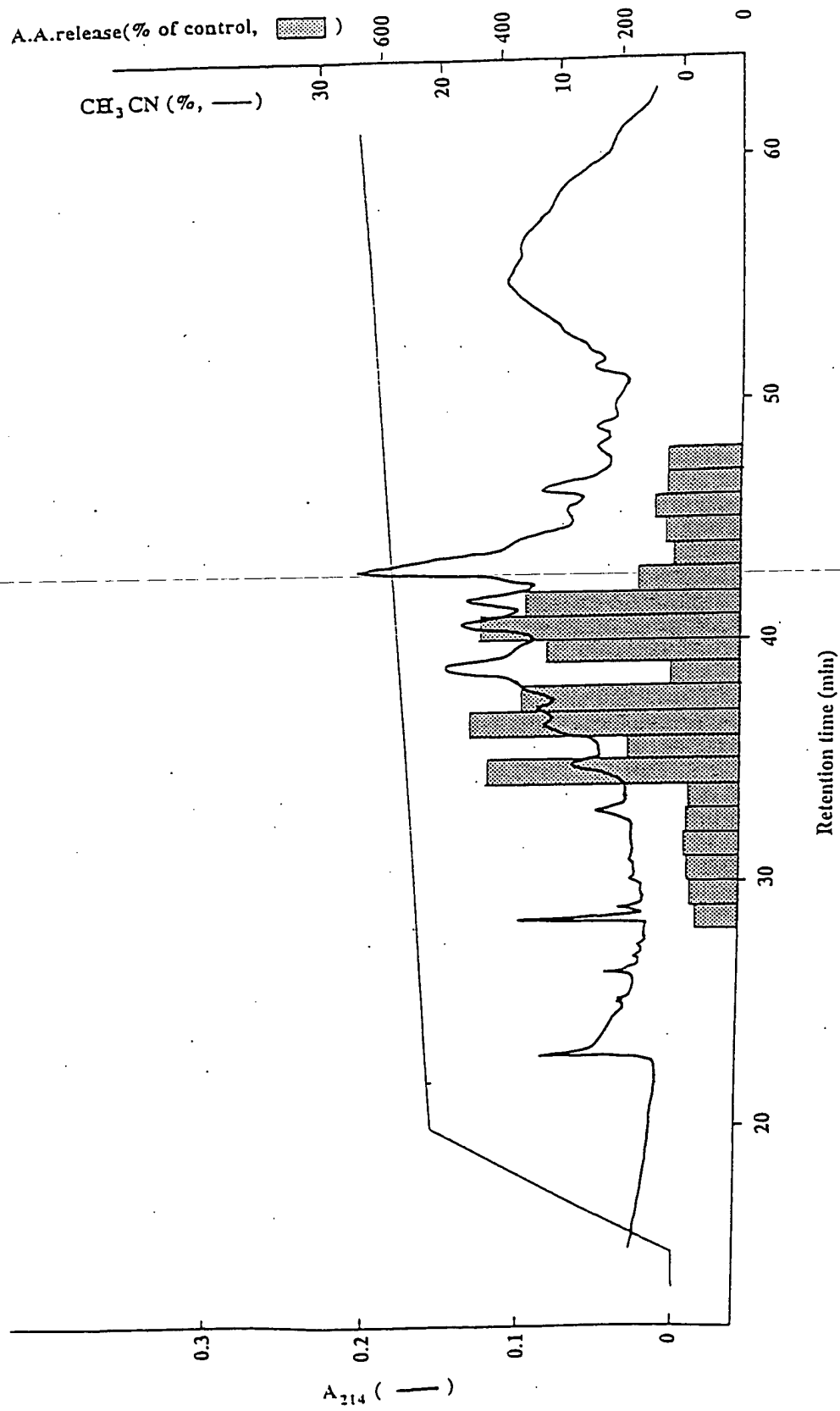
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Fig. 17



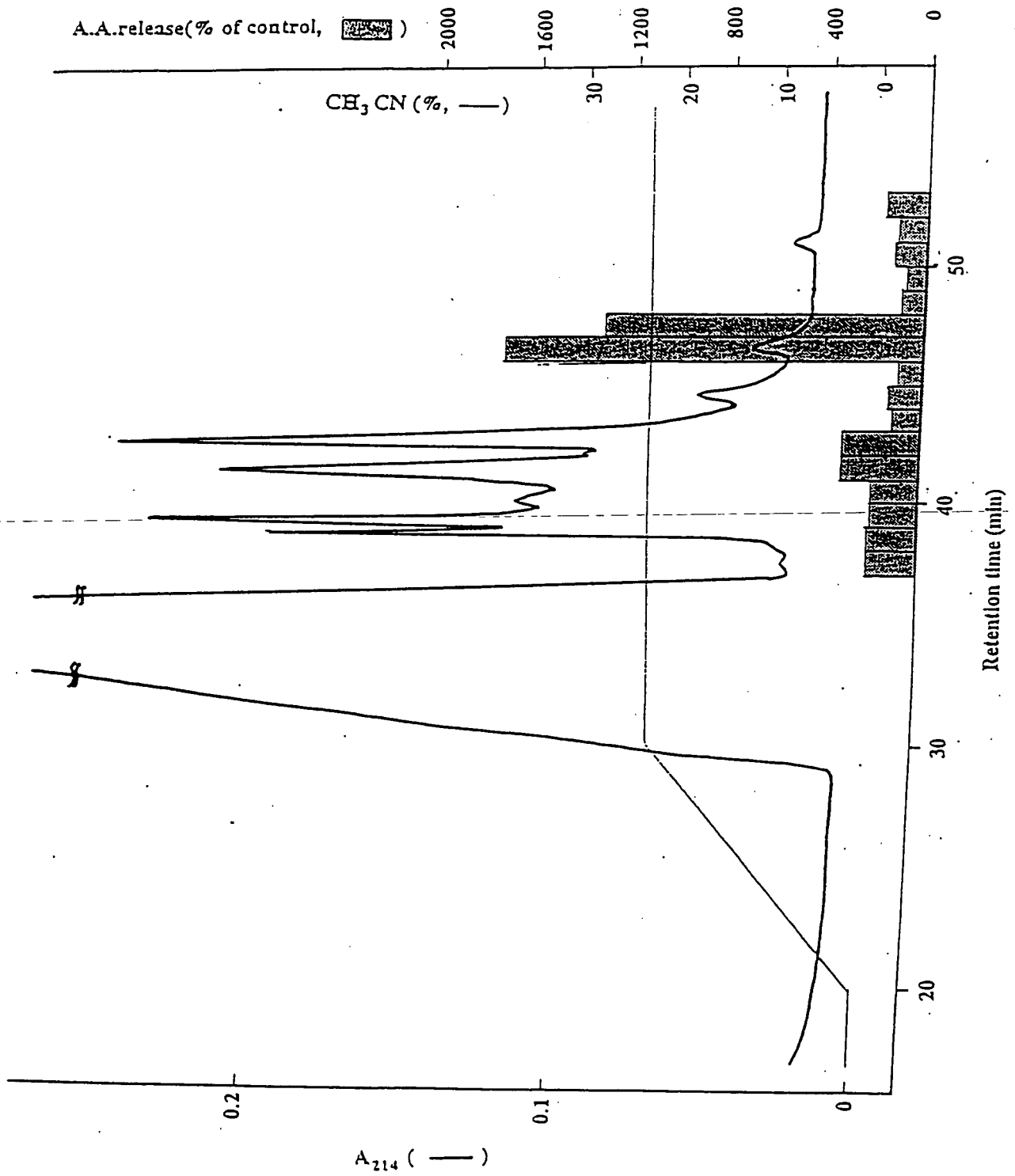
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Fig. 18



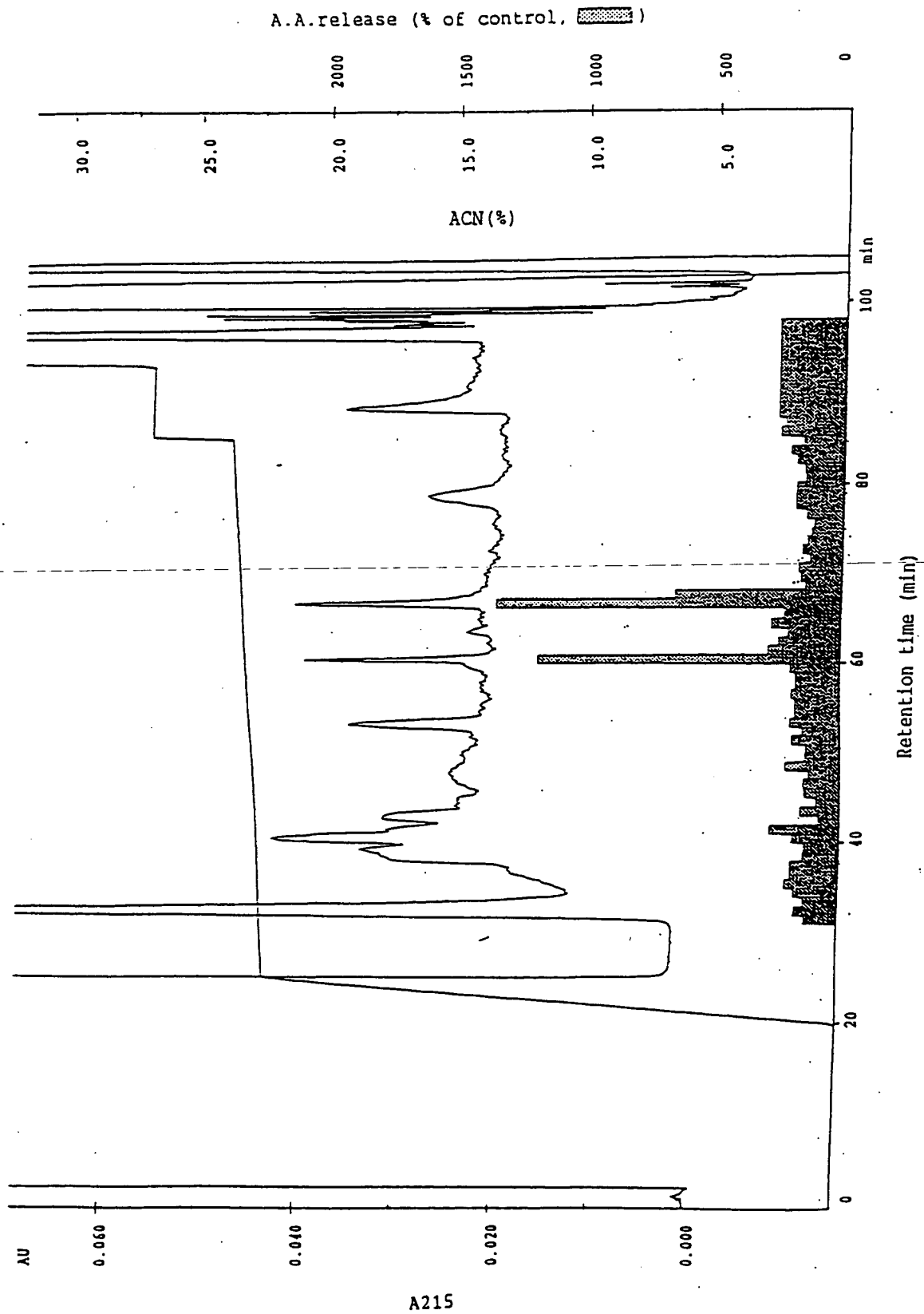
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Fig. 19



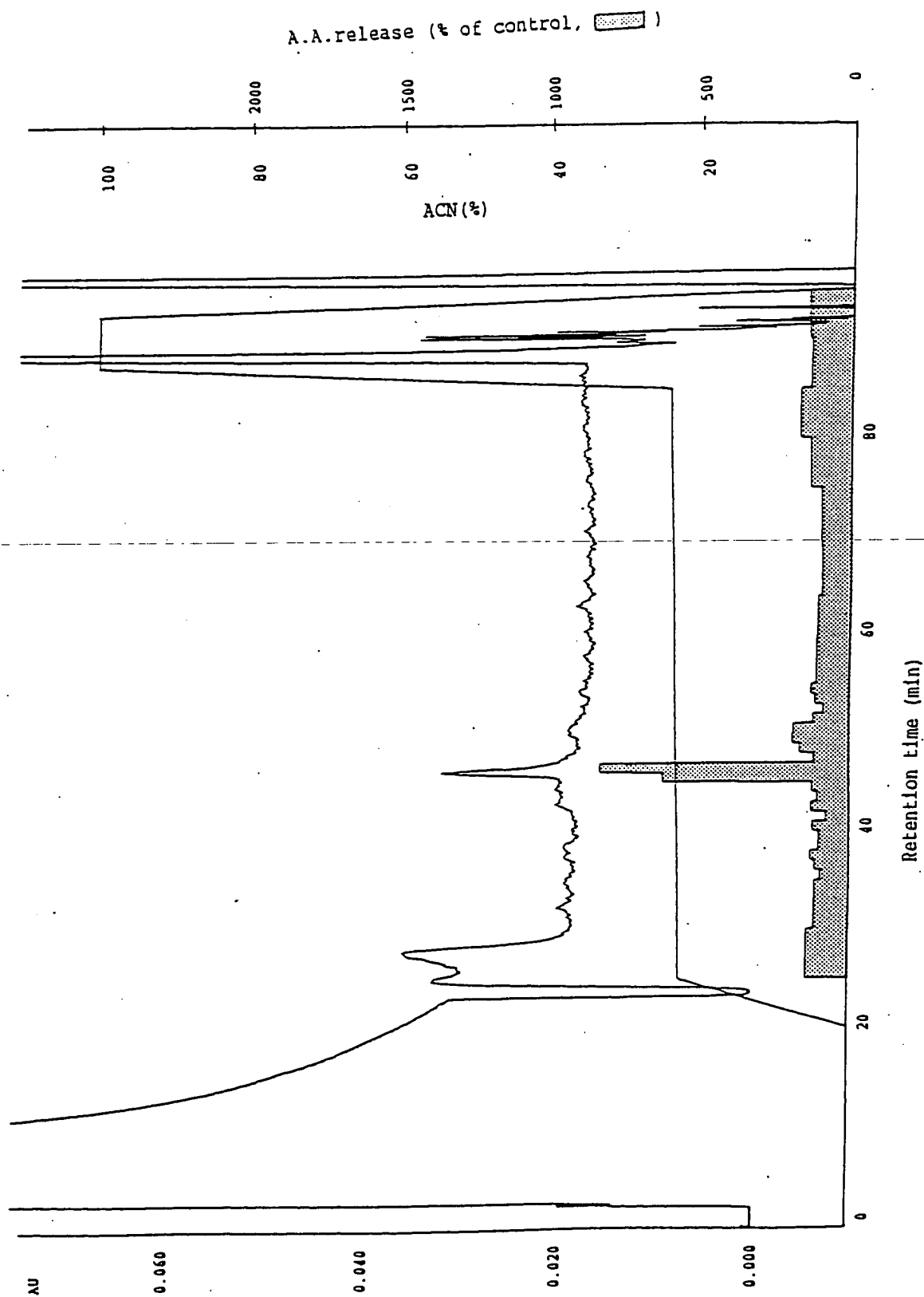
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Fig. 20



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Fig. 21



A215

[illegible]

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Fig. 24(a)

1 GTGGAATGAAGGCGGTGGGGGCCTGGCTCCTCTGCCTGCTGCTGCTGGGCCTGGCCCTG 59
1 MetLysAlaValGlyAlaTrpLeuLeuCysLeuLeuLeuGlyLeuAlaLeu 18

60 CAGGGGGCTGCCAGCAGAGCCCACCAGCACTCCATGGAGATCCGCACCCCCGACATCAAC 119
19 GlnGlyAlaAlaSerArgAlaHisGlnHisSerMetGluIleArgThrProAspIleAsn 38

120 CCTGCCTGGTACGCRGGCCGTGGGATCCGGCCCGTGGGCCTCGCTTCGGCCGGCGAAGAGCT 179
39 ProAlaTrpTyrAlaGlyArgGlyIleArgProValGlyArgPheGlyArgArgArgAla 58

180 GCCCCGGGGGACGGACCCAGGCCTGGCCCCCGGCGTGTGCCGGCCTGCTTCCGCCTGGAA 239
59 AlaProGlyAspGlyProArgProGlyProArgArgValProAlaCysPheArgLeuGlu 78

240 GCGGGYGCTGAGCCCTCCCGAGCCCTCCCGGGGCGGCTGACGGCCCAGCTGGTCCAGGAA 299
79 GlyGlyAlaGluProSerArgAlaLeuProGlyArgLeuThrAlaGlnLeuValGlnGlu 98

300 TAACAGCGGGAGCCTGCCCCCACCCTCCTCCTCCACCAGCCACCTTCCCTCCAGTCCT 359
98 98

360 AATAAAAGCAGCTGGCTTGTT 380
98 98

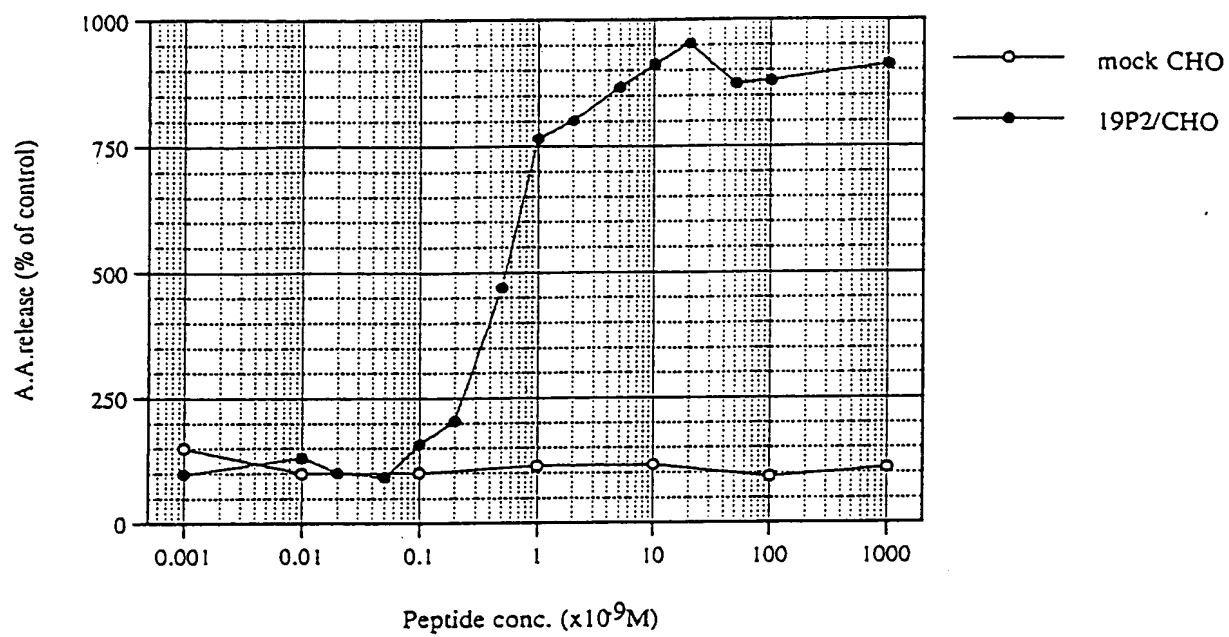
Fig. 24(b)

1	GTGGAATGAAGGCGGTGGGGGCTGGCTCCTCTGCCTGCTGCTGGGCTGGCCATG	59
1	MetLysAlaValGlyAlaTrpLeuLeuCysLeuLeuLeuLeuGlyLeuAlaLeu	18
60	CAGGGGGCTGCCAGCAGAGCCCACCAGCACTCCATGGAGATCCGCACCCCCGACATCAAC	119
19	GlnGlyAlaAlaSerArgAlaHisGlnHisSerMetGluIleArgThrProAspIleAsn	38
120	CCTGCCTGGTACGCRGGCCGTGGGATCCGGCCCCGTGGGCTGCTTCGGCCGGCGAAGAGCT	179
39	ProAlaTrpTyrAlaGlyArgGlyIleArgProValGlyArgPheGlyArgArgArgAla	58
180	GCCCTGGGGGACGGACCCAGGCCTGGCCCCCGGCGTGTGCCGGCCTGCTTCCGCCTGGAA	239
59	AlaLeuGlyAspGlyProArgProGlyProArgArgValProAlaCysPheArgLeuGlu	78
240	GGCGGYGCTGAGCCCTCCCGAGCCCTCCCGGGGCGGCTGACGGCCCAGCTGGTCCAGGAA	299
79	GlyGlyAlaGluProSerArgAlaLeuProGlyArgLeuThrAlaGlnLeuValGlnGlu	98
300	TAACAGCGGGAGCCTGCCCCCACCCTCCTCCTCCACCAGCCACCTTCCCTCCAGTCCT	359
98		98
360	AATAAAAGCAGCTGGCTTGTT	380
98		98

[illegible]

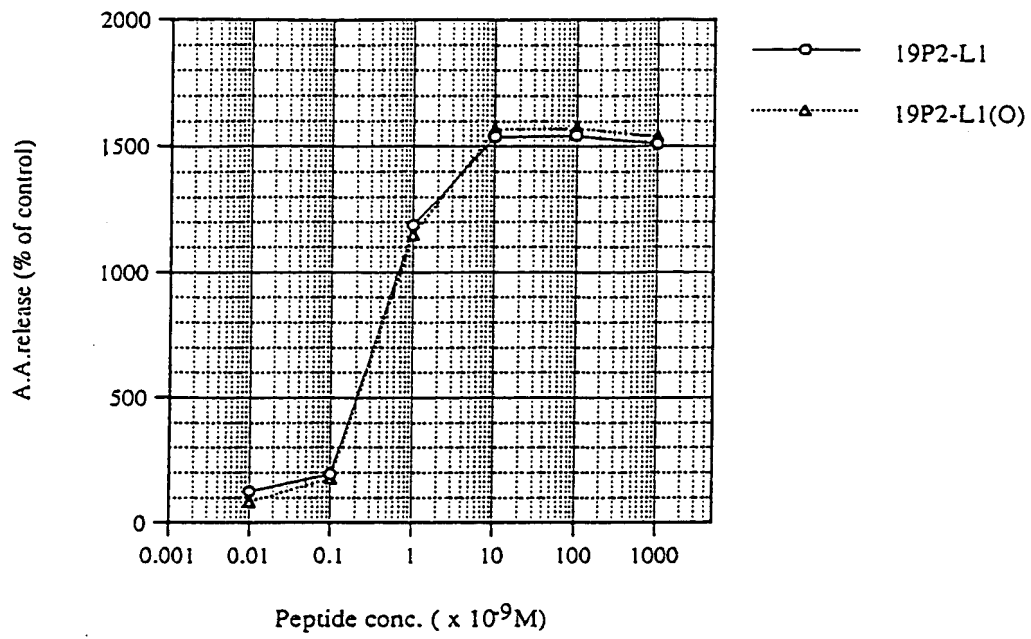
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Fig. 25



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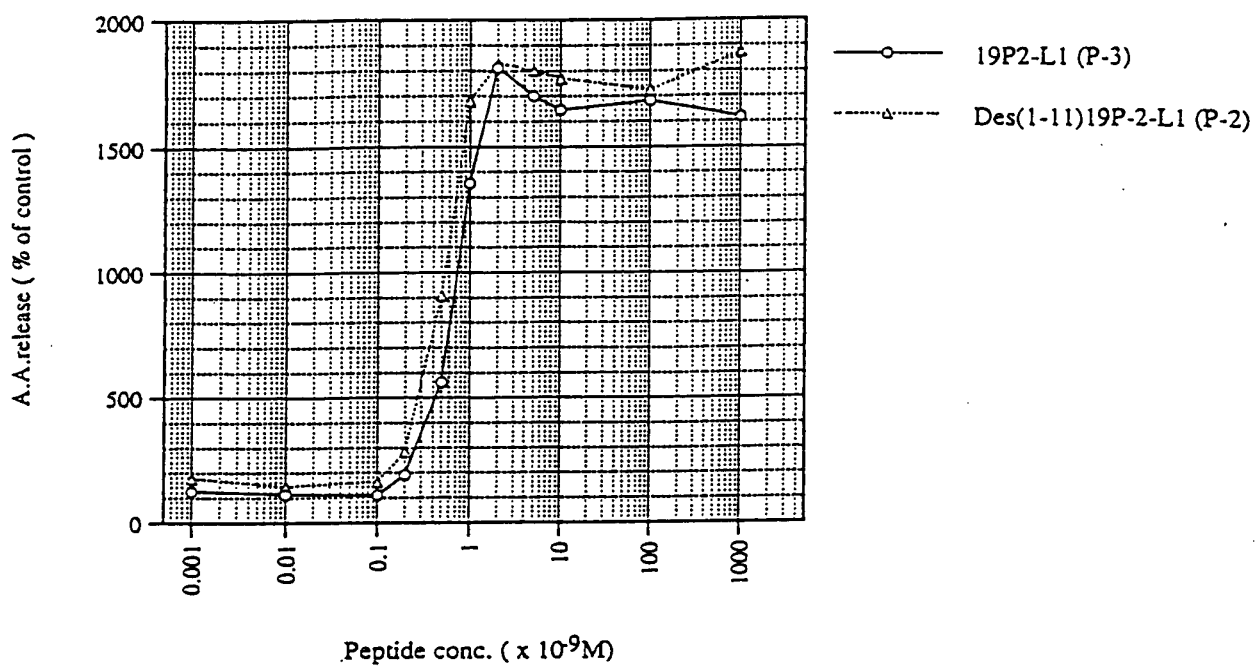
Fig. 26



660227-41551160

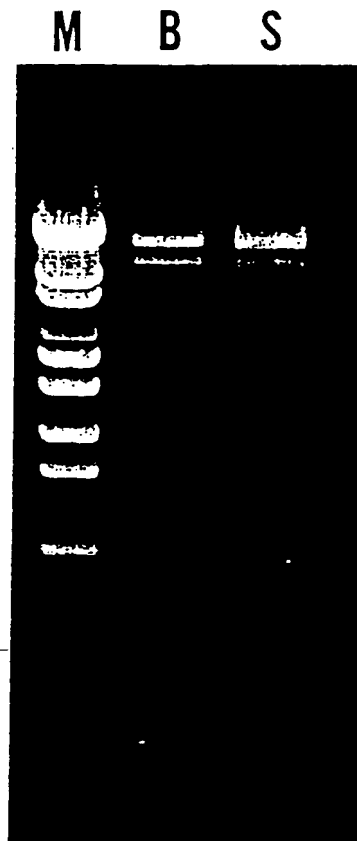
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Fig. 27



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Fig. 28



660227-459460-

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Fig. 29

10	20	30	40	50	60
ATGAAGGCGG	TGGGGGCCTG	GCTCCTCTGC	CTGCTGCTGC	TGGGCCTGGC	CCTGCAGGGG
70	80	90	100	110	120
GCTGCCAGCA	GAGCCCACCA	GCACTCCATG	GAGATCCGCA	GTGAGTGTCT	AGCCCCGCCC
130	140	150	160	170	180
CTGCCCCCAG	GGGTCACAGG	GGGGGCCTGG	CCACTTCCTG	GGCTGGGACA	TCCTTGCTAA
190	200	210	220	230	240
GCATCCTGGG	GTGTTGGGTTT	GGCCTCCTGT	TCCCCAGACC	CTTCCCCCAG	GTGGCCCCGA
250	260	270	280	290	300
CAGGTGCTCC	CAAGGGTCCC	GGCCCAGCAC	ACGGGGGAGG	GTCATCCTC	ACCACACGGG
310	320	330	340	350	360
TGGCCTGGGG	CTGAGTGCAC	GTCACCCATG	AGAACGGGGC	TGTGAGGACA	GGAAAGGAAG
370	380	390	400	410	420
GGGAGTGTGT	CCTGGTGTGA	GTCTGAAATC	CTACTTCCCA	AAGCCACCCC	AGCACCAGAA
430	440	450	460	470	480
ATGGGCGCTC	CGGGTGAACC	TCCTGTGCGG	GTGGGTGGTC	CTGGCATGGC	CTGGGCGACA
490	500	510	520	530	540
GGCAGCCATG	AGCTGAGCAC	ACACCCGGCC	CGGCCACCAG	GGCTGTATGC	TCCAGGGCAC
550	560	570	580	590	600
AGGCCTCCAT	GCGCTCTTCT	CTCTCTTTCC	AGCCCCCGAC	ATCAACCCTG	CCTGGTACGC
610	620	630	640	650	660
AGGCCGTGGG	ATCCGGCCCCG	TGGGCCGCTT	CGGCCGGCGA	AGAGCTGCCC	TGGGGGACGG
670	680	690	700	710	720
ACCCAGGCCT	GGCCCCCGGC	GTGTGCCCGC	CTGCTTCCGC	CTGGAAGGCG	GTGCTGAGCC
730	740	750	760	770	780
CTCCCGAGCC	CTCCCGGGGC	GGCTGACGGC	CCAGCTGGTC	CAGGAATAA.

Fig. 30

genome cDNA	1	10	20	30	40	50	
	1	ATGAAGGCGG	TGGGGGCCTG	GCTCCTCTGC	CTGCTGCTGC	TGGGCCTGGC	50
genome cDNA	51	60	70	80	90	100	
	51	CCTGCAGGGG	GCTGCCAGCA	GAGCCCACCA	GCACTCCATG	GAGATCCGCA	100
genome cDNA	101	110	120	130	140	150	
	101	GTGAGTGTCT	AGCCCCGCCC	CTGCCCCCAG	GGGTACACAG	GGGGGCCTGG	150
genome cDNA	151	160	170	180	190	200	
	151	CCACTTCCTG	GGCTGGGACA	TCCTTGCTAA	GCATCCTGGG	GTTGGGGTTT	200
genome cDNA	201	210	220	230	240	250	
	201	GGCCTCCTGT	TCCCCAGACC	CTTCCCCCAG	GTGGCCCGGA	CAGGTGCTCC	250
genome cDNA	251	260	270	280	290	300	
	251	CAAGGGTCCC	GGCCCAGCAC	ACGGGGGAGG	GTCACCTCCT	ACCACACGGG	300
genome cDNA	301	310	320	330	340	350	
	301	TGGCCTGGGG	CTGAGTGCAC	GTCACCCATG	AGAACGGGGC	TGTGAGGACA	350
genome cDNA	351	360	370	380	390	400	
	351	GGAAAGGAAG	GGGAGTGTGT	CCTGGTGTGA	GTCTGAAATC	CTACTTCCCA	400
genome cDNA	401	410	420	430	440	450	
	401	AAGCCACCCC	AGCACCAGAA	ATGGGCGCTC	CGGGTGAACC	TCCTGTGCGG	450
genome cDNA	451	460	470	480	490	500	
	451	GTGGGTGGTC	CTGGCATGGC	CTGGGCGACA	GGCAGCCATG	AGCTGAGCAC	500
genome cDNA	501	510	520	530	540	550	
	501	ACACCCGGCC	CGGCCACCAG	GGCTGTATGC	TCCAGGGCAC	AGGCCTCCAT	550
genome cDNA	551	560	570	580	590	600	
	551	GCGCTCTTCT	CTCTCTTTCC	AGCCCCCGAC	ATCAACCCTG	CCTGGTACGC	600
genome cDNA	601	610	620	630	640	650	
	601	AGGCCGTGGG	ATCCGGCCCCG	TGGGCCGCTT	CGGCCGGCGA	AGAGCTGCCC	650
genome cDNA	651	660	670	680	690	700	
	651	TGGGGGACGG	ACCCAGGCCT	GGCCCCCGGC	GTGTGCCGGC	CTGCTTCCGC	700
genome cDNA	701	710	720	730	740	750	
	701	CTGGAAGGCG	GTGCTGAGCC	CTCCCGAGCC	CTCCCGGGGC	GGCTGACGGC	750
genome cDNA	751	760	770	780	790	800	
	751	CCAGCTGGTC	CAGGAATAA.	800

[illegible]

bovine.aa		M K A V G A W L L			
		10 20 30 40 50			
bovine.seq	-18	GT GGAATGAAGG CCGTGGGGGC CTGGCTCCTC	32		
rat.seq	1 GGCATCATCC AGGAAGACGG AGCATG---G CCCTGAAGAC GTGGCTCTCTG	50			
<hr/>					
bovine.aa	C L L L L G L A L Q G A A S R A H				
	60 70 80 90 100				
bovine.seq	33 TGCTTGCTGC TGCTGGGCCCT GGCCCTGCAG GGGGCTGCCA GCAGAGCCCCA	82			
rat.seq	51 TGCTTGCTGC TGCTAAAGCTT GGTCTCTCCA GGGGCTTCCA GCCGAGCCCCA	100			
	R1				
bovine.aa	Q H S M E I R T P D I N P A W Y A				
	110 120 130 140 150				
bovine.seq	83 CCAGCACTCC ATGGAGATCC GCACCCCCGA CATCAACCCT GCCTGGTACG	132			
rat.seq	101 CCAGCACTCC ATGGAGACAA GAACCCCTGA TATCAATCTT GCCTGGTACA	150			
	R3				
bovine.aa	G R G I R P V G R F G R R R A A				
	160 170 180 190 200				
bovine.seq	133 CGGGCCGTTG GATCCGGCCC GTGGGCCGCT TCGGCCGGCG AAGAGCTGCC	182			
rat.seq	151 CGGGCCGCGG GATCAGGCCT GTGGGCCGCT TCGGCAGGAG AAGGGCAACC	200			
	R4				
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bovine.seq	183 CCGGGGGACG GACCCAGGCC TGGCCCCCGG CGTGTCGCCG CCTGCTTCCG	232			
rat.seq	201 CCGAGGGATG TCACTGGACT TGCC----- ---CAACTCA GCTGCCTCCC	250			
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bovine.aa	L E G G A E P S R A L P G R L T A				
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rat.seq	251 ACTGGATGGA CGCACCAAGT TCTCTCAGCG TGATAACAC CCCAGCTCGA	300			
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bovine.aa	Q L V Q E *				
	310 320 330 340 350				
bovine.seq	283 CCCAGCTGGT CCAGGAATAA CAGCGGGAGC CTGCCCCCA CCCCTCTCTC	332			
rat.seq	301 GAAGACAGTG CTGCTGAGCC CAAGCCCACA CTCCTGTCTC CCTGCAGACC	350			
	360 370 380 390 400				
bovine.seq	333 TCCACCAGCC ACCTTCCCTC CAGTCCTAAT AAAAGCAGCT GGCTTGTT..	382			
rat.seq	351 CTCCTCTACC CTCCCTCTCC TCTGCT....	400			

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Fig. 34

1	GGCCTCCTCGGAGGAGCCAAGGGATGAAGGTGCTGAGGGCCTGGCTCCTGTGCCTGCTG	59
1	MetLysValLeuArgAlaTrpLeuLeuCysLeuLeu	12
60	ATGCTGGGCCTGGCCCTGCGGGGAGCTGCAAGTCGTACCCATCGGCACTCCATGGAGATC	119
13	MetLeuGlyLeuAlaLeuArgGlyAlaAlaSerArgThrHisArgHisSerMetGluIle	32
120	CGCACCCCTGACATCAATCCTGCCTGGTACGCCAGTCGCGGGATCAGGCCTGTGGGCCGC	179
33	ArgThrProAspIleAsnProAlaTrpTyrAlaSerArgGlyIleArgProValGlyArg	52
180	TTCGGTCGGAGGAGGGCAACCCTGGGGGACGTCCCCAAGCCTGGCCTGCGACCCCGGCTG	239
53	PheGlyArgArgArgAlaThrLeuGlyAspValProLysProGlyLeuArgProArgLeu	72
240	ACCTGCTTCCCCCTGGAAGGCGGTGCTATGTCGTCCCAGGATGGCTGACAGCCAGCTTGT	299
73	ThrCysPheProLeuGluGlyGlyAlaMetSerSerGlnAspGly***	87
300	CAAGAACTCACTCTGGAGCCTCCCCACCCACCCCTCTCCTCTCCTTCGGGCTCCTTTC	359
87		87
360	CC	361
87		87

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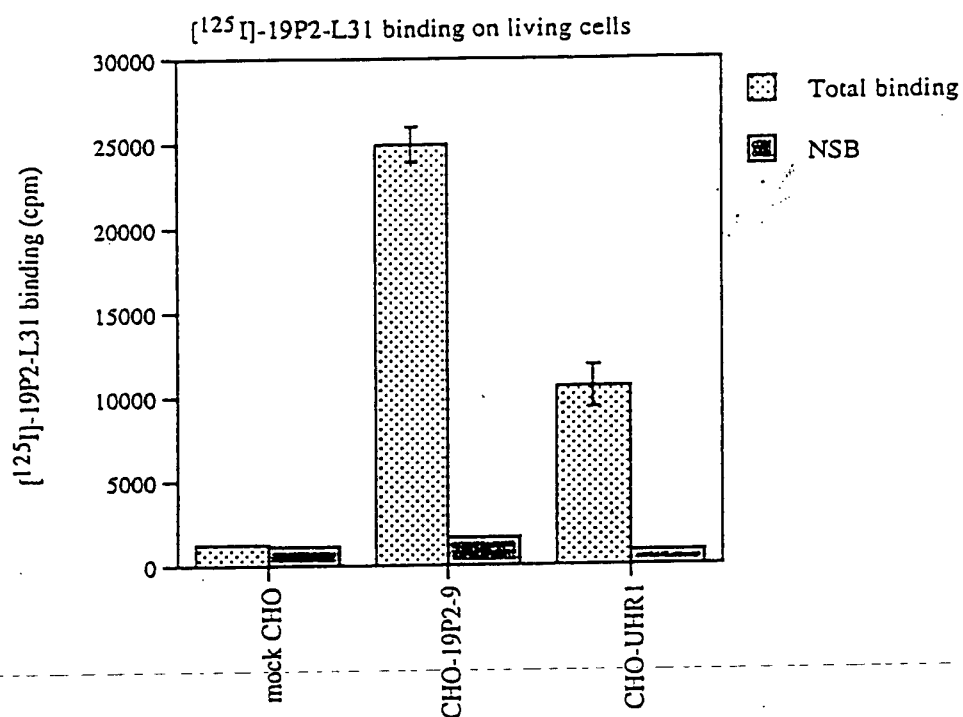
Fig. 35

	10	20	30	40	50	
bovine.aa	1 MKAVGAWLLC	LLLLGLALQG	AASRAHQHSM	EIRTPDINPA	WYAGRGIRPV	50
rat.aa	1 M-ALKTWLLC	LLLLSLVLPG	ASSRAHQHSM	ETRTPDINPA	WYTGRGIRPV	50
human.aa	1 MKVLRAWLLC	LLMLGLALRG	AASRTHRHSM	EIRTPDINPA	WYASRGIRPV	50
	60	70	80	90	100	
bovine.aa	51 GRFGRRRAAP	GDGPRPGPRR	VPACFRLEGG	AEPSRALPGR	LTAQLVQE*.	100
rat.aa	51 GRFGRRRATP	RDVTGLG---	QLSCLPLDGR	TKFSQRG*..	100
human.aa	51 GRFGRRRATL	GDVFKPGLRP	RLTCFPLEGG	AMSSQDG*..	100

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Fig. 36

cells; 0.5×10^7 cells/ml[¹²⁵I]-19P2-L31; 200pM (avg. 63857.3cpm)

NSB; 200nM (x 1,000)

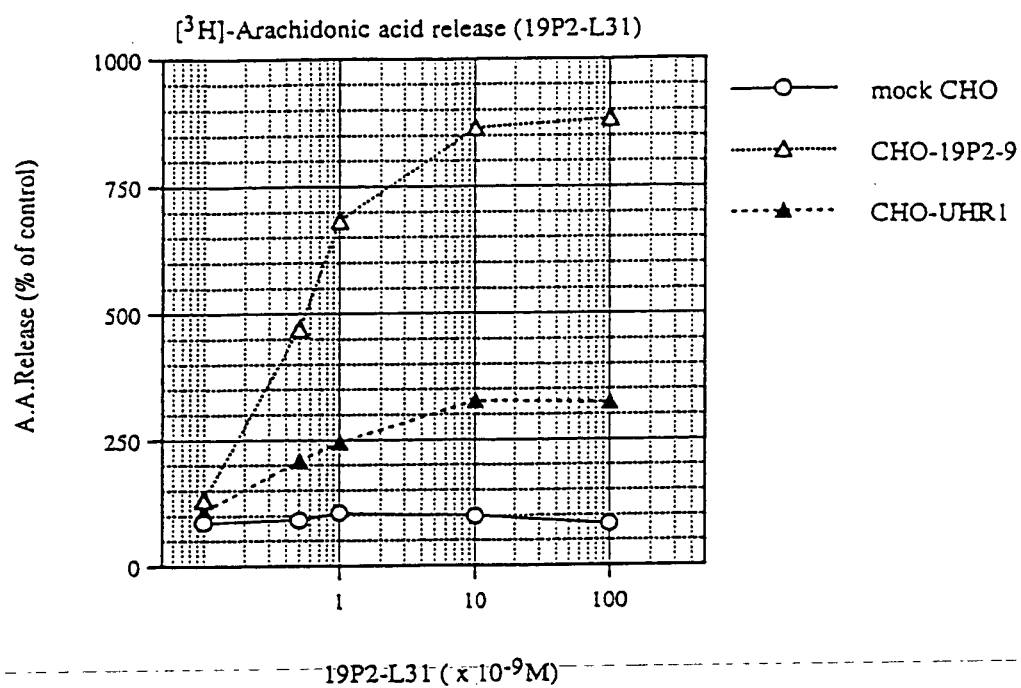
reaction; RT, 2.5hr

in HBSS + 0.05% BSA + 0.05% CHAPS

in 100 μ l

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Fig. 37



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Fig. 38

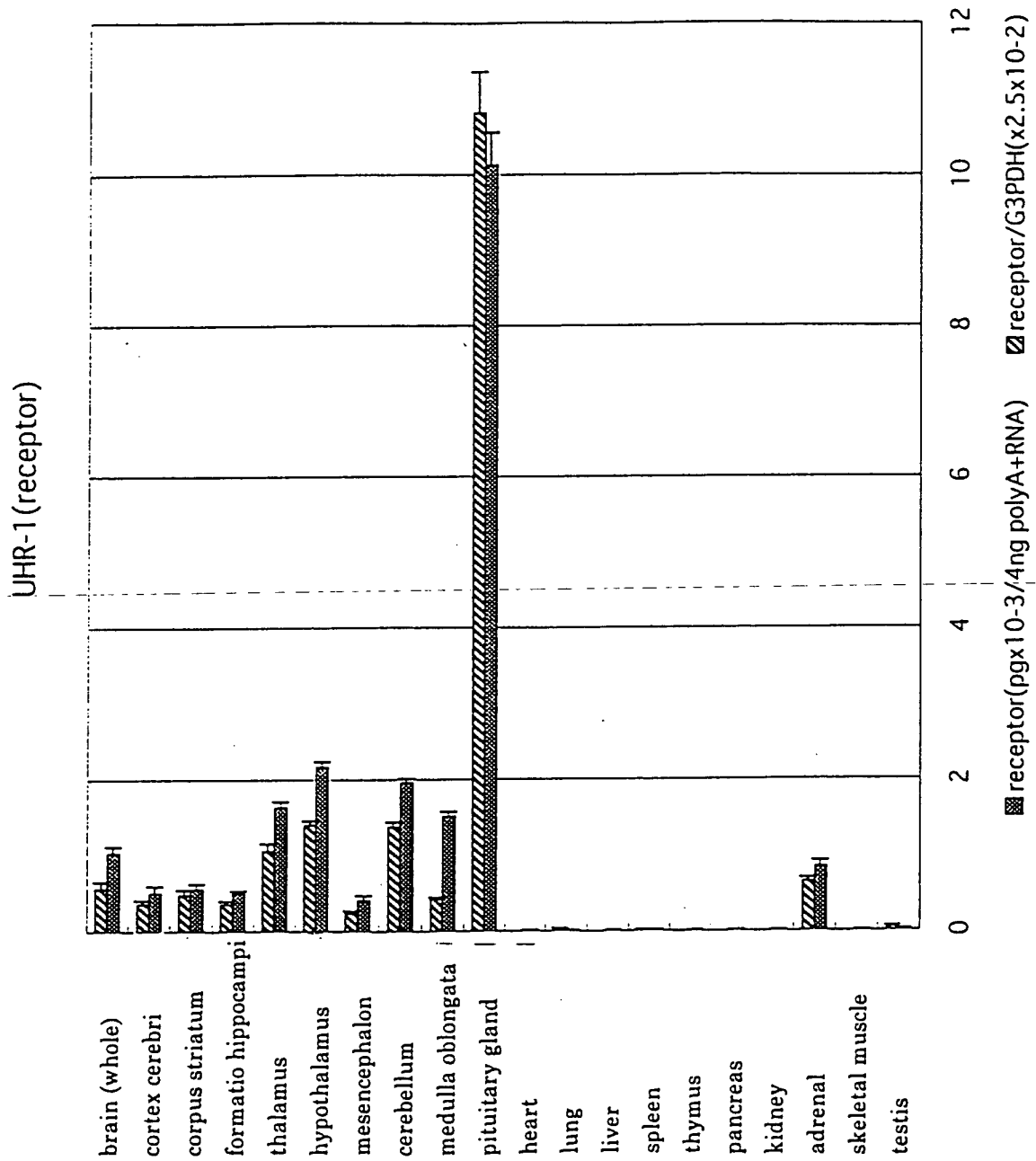
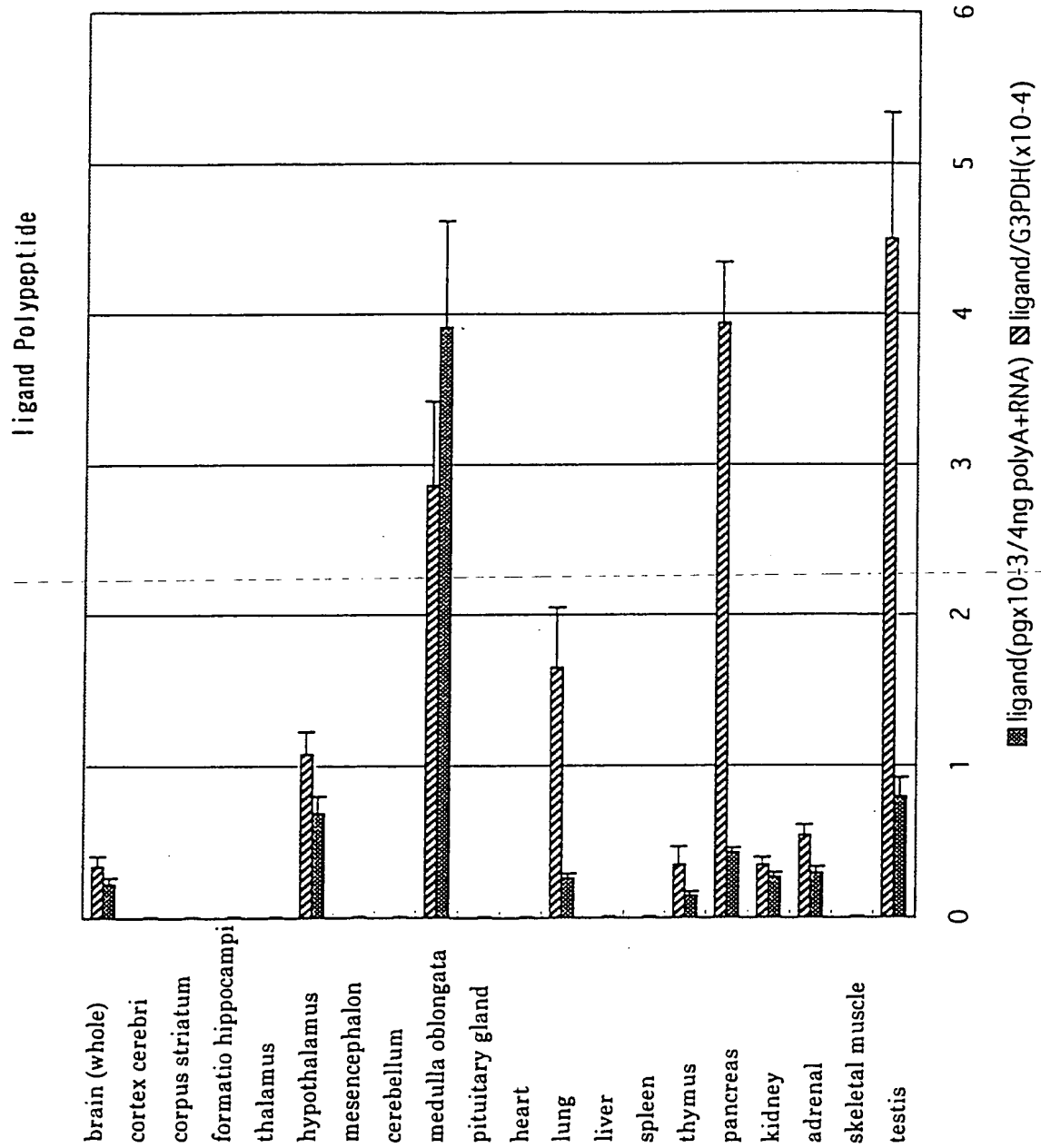


Fig. 39



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Fig. 40

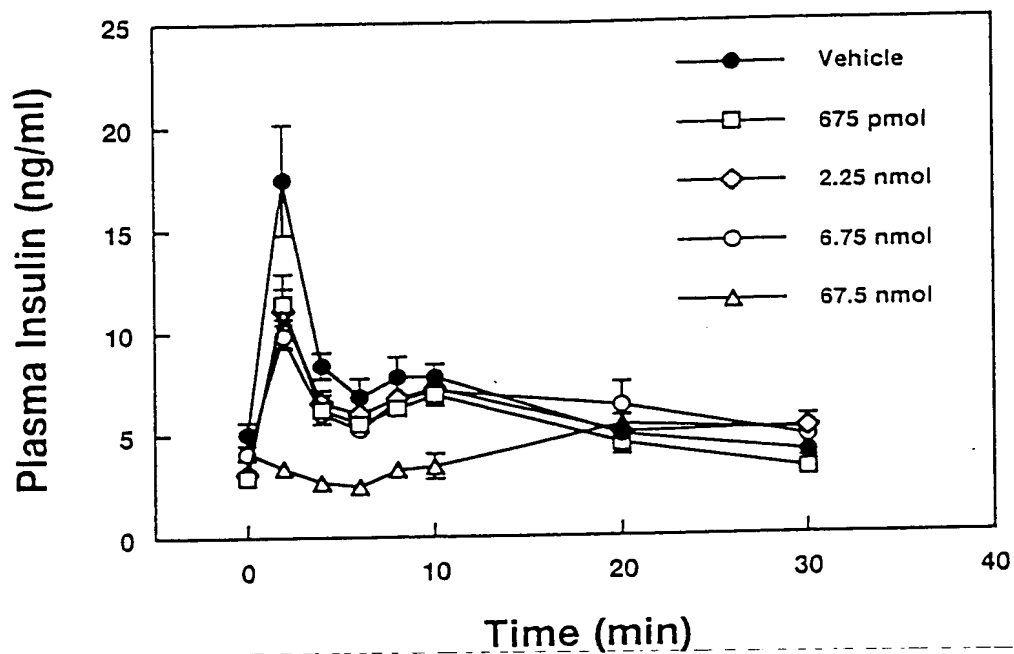
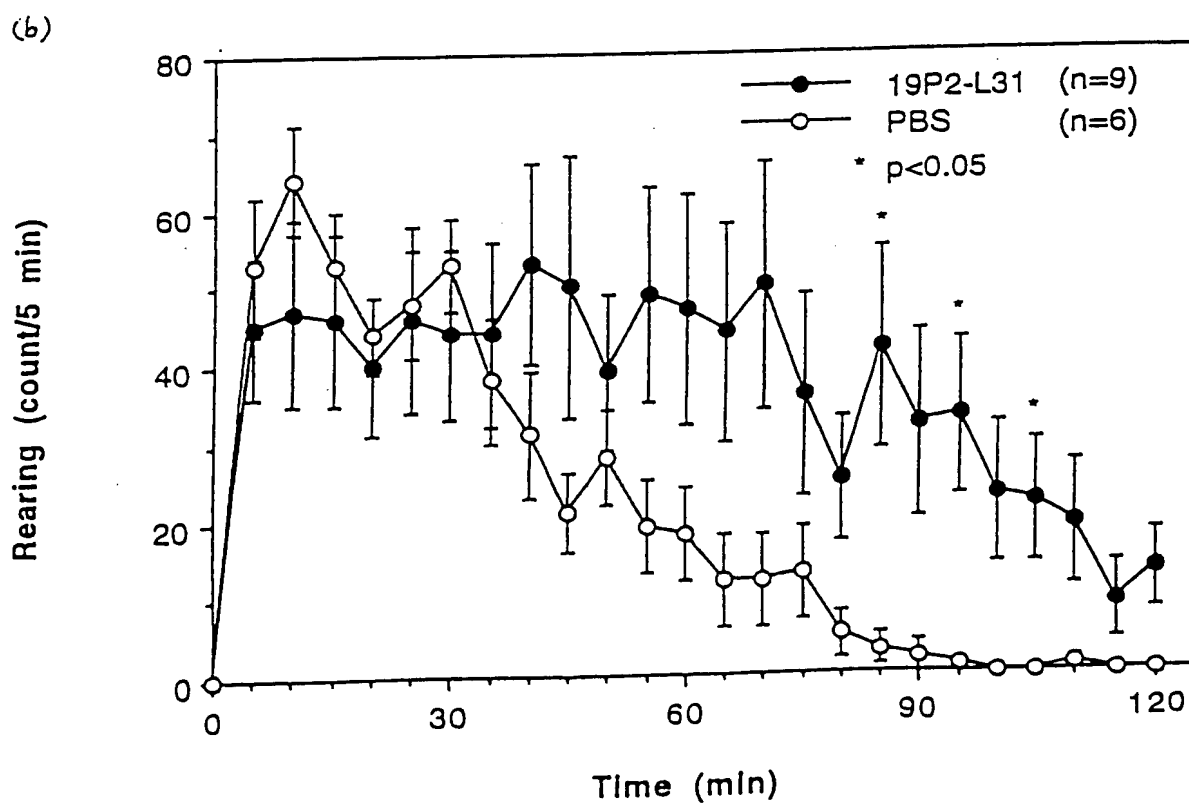
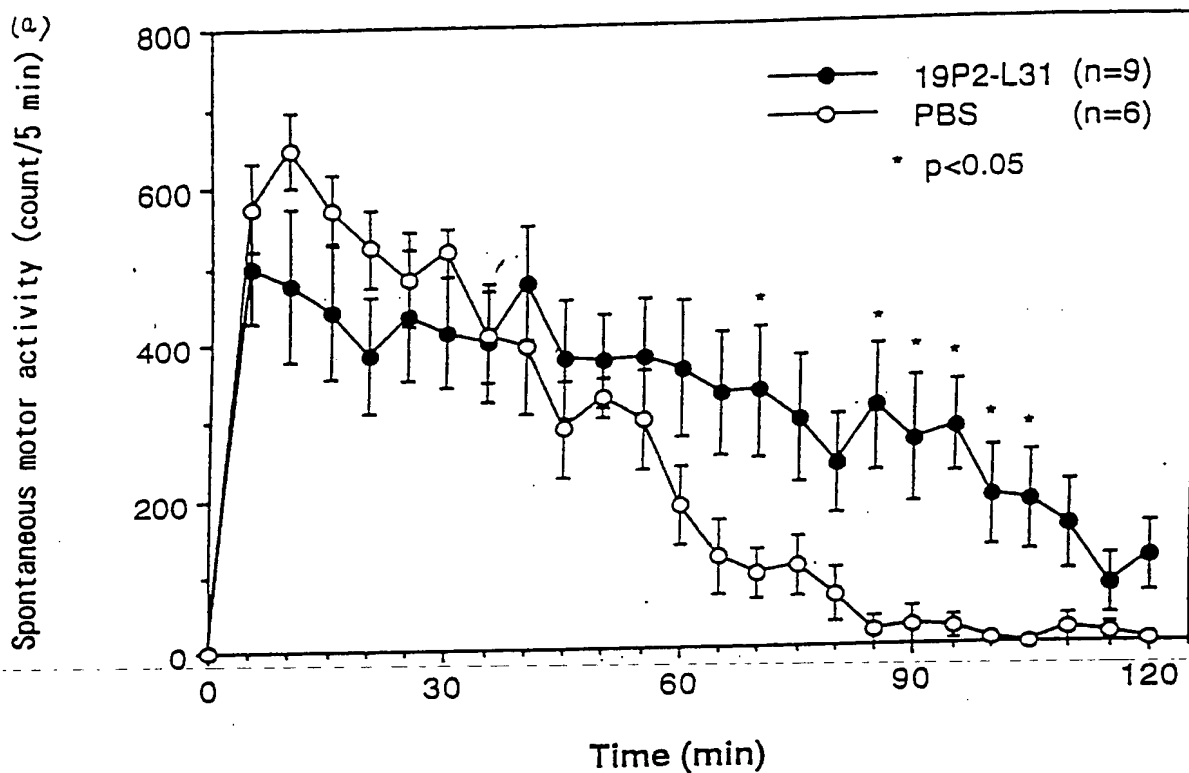
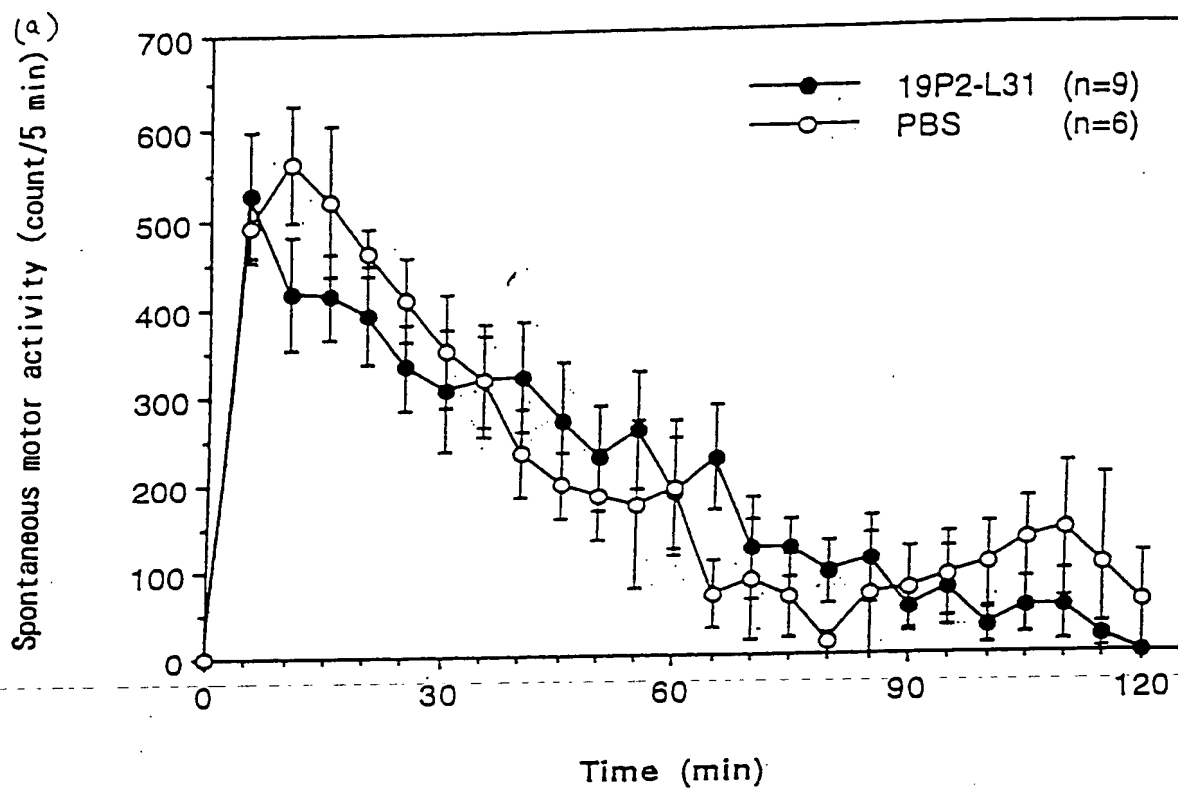


Fig. 41

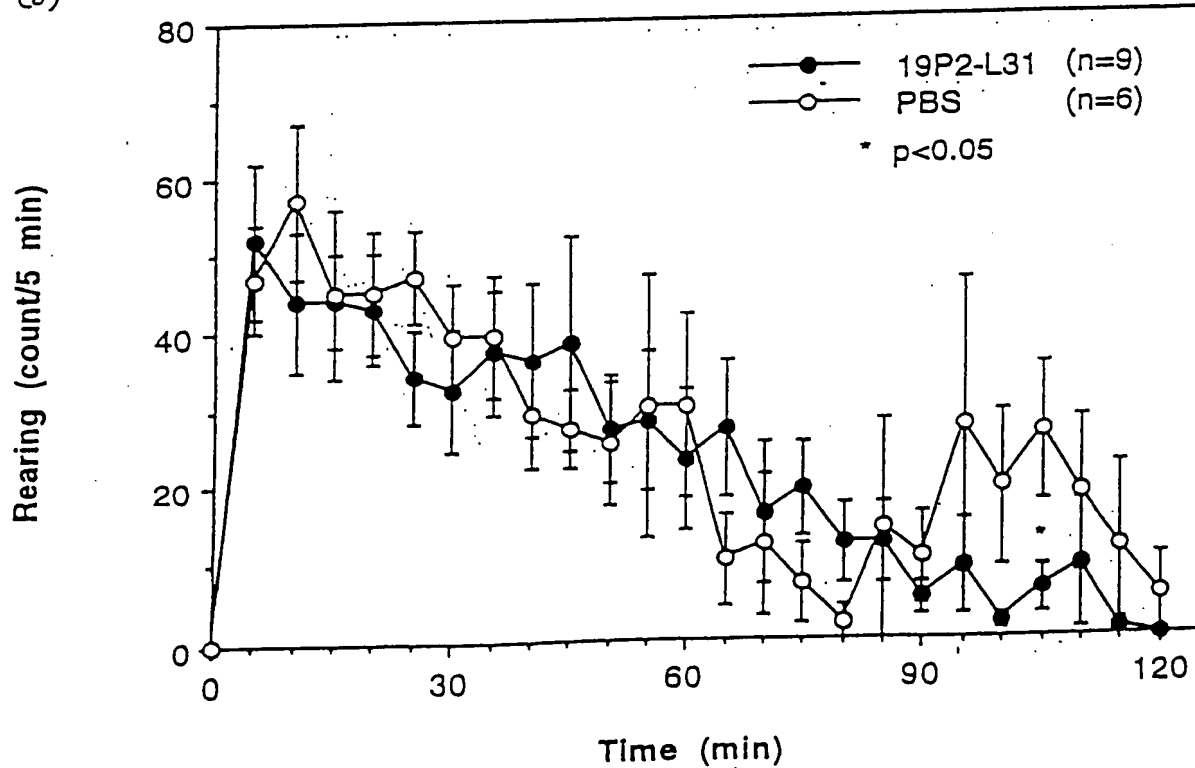


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Fig. 42

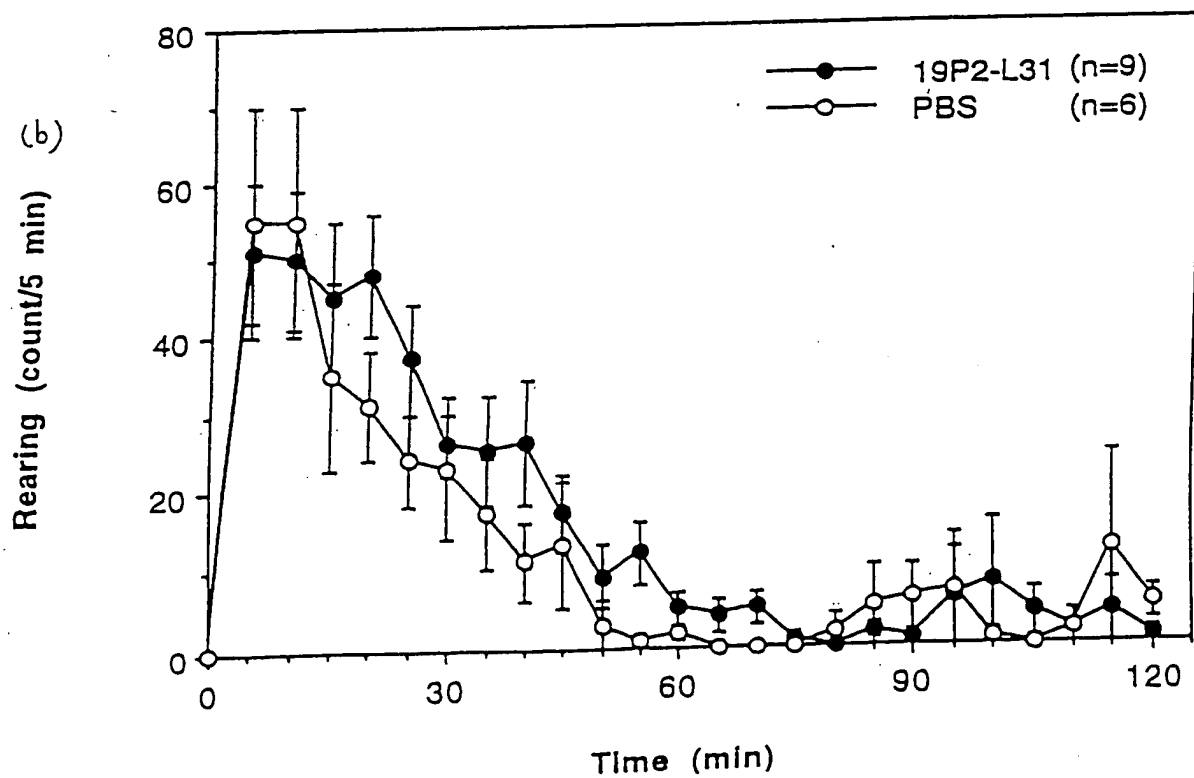
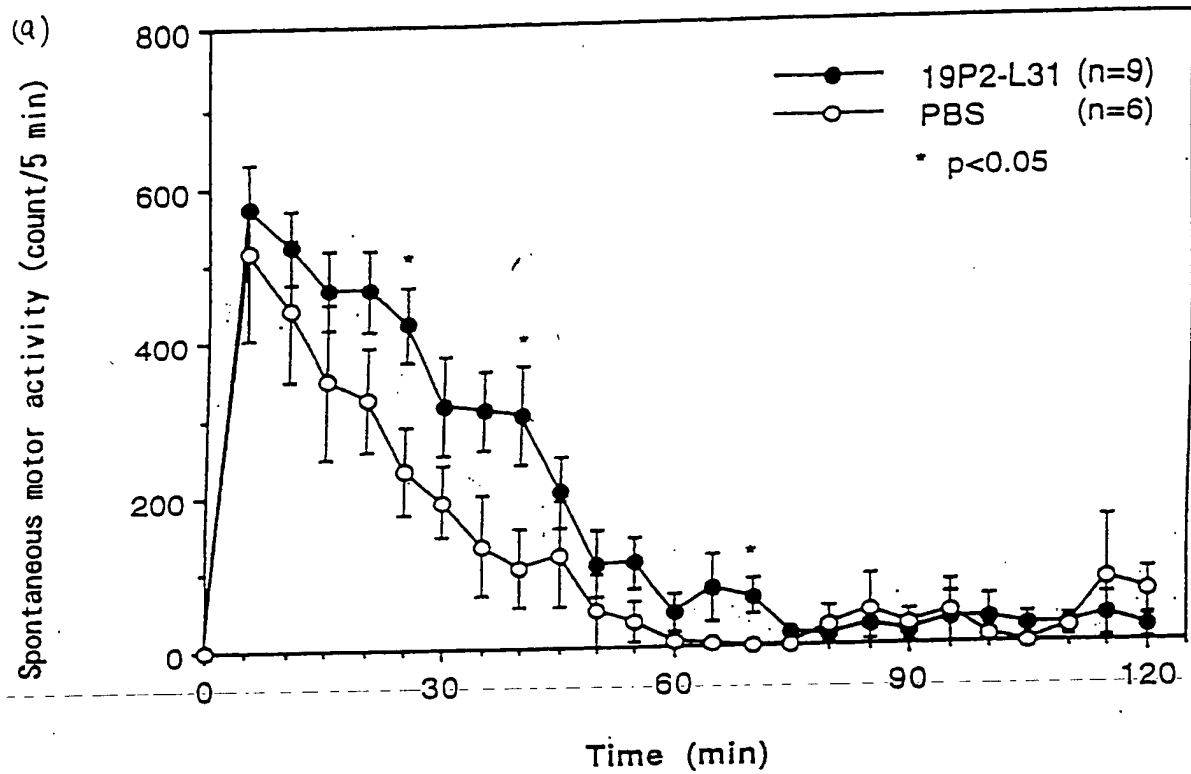


(b)



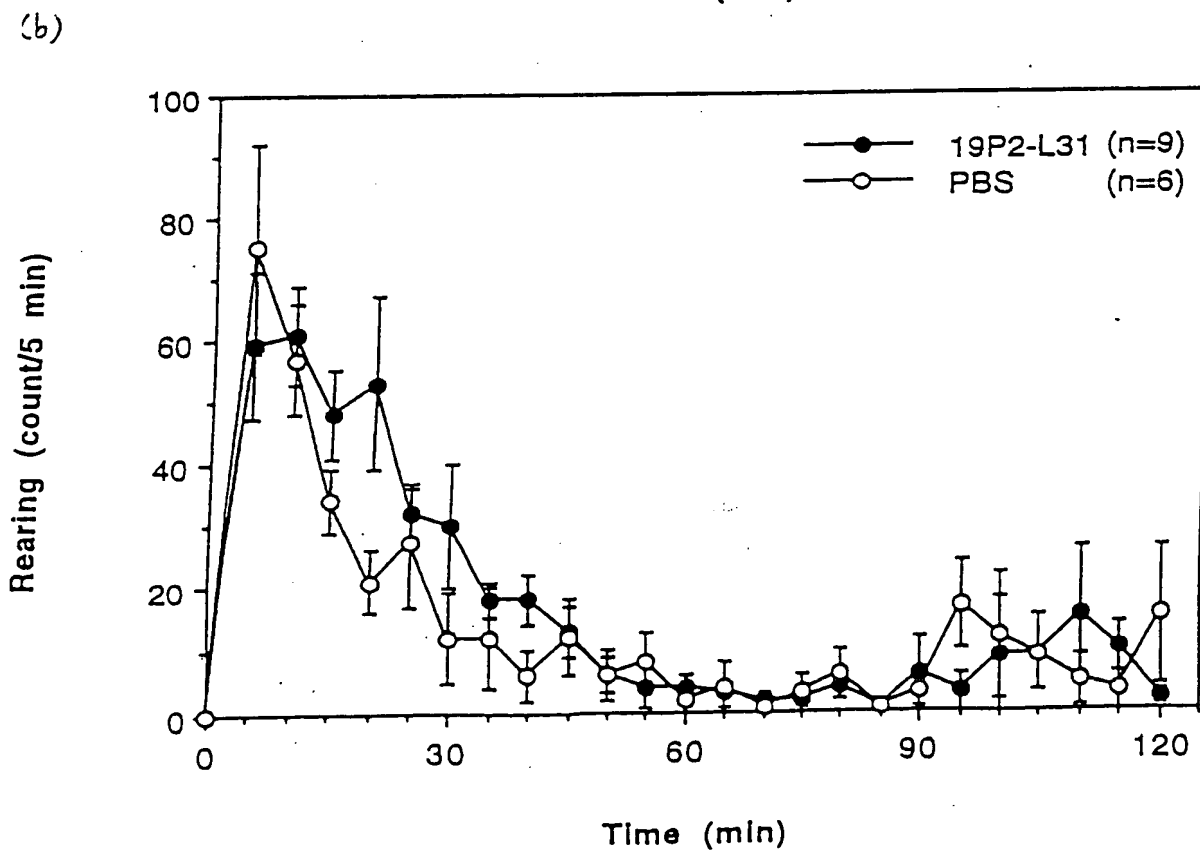
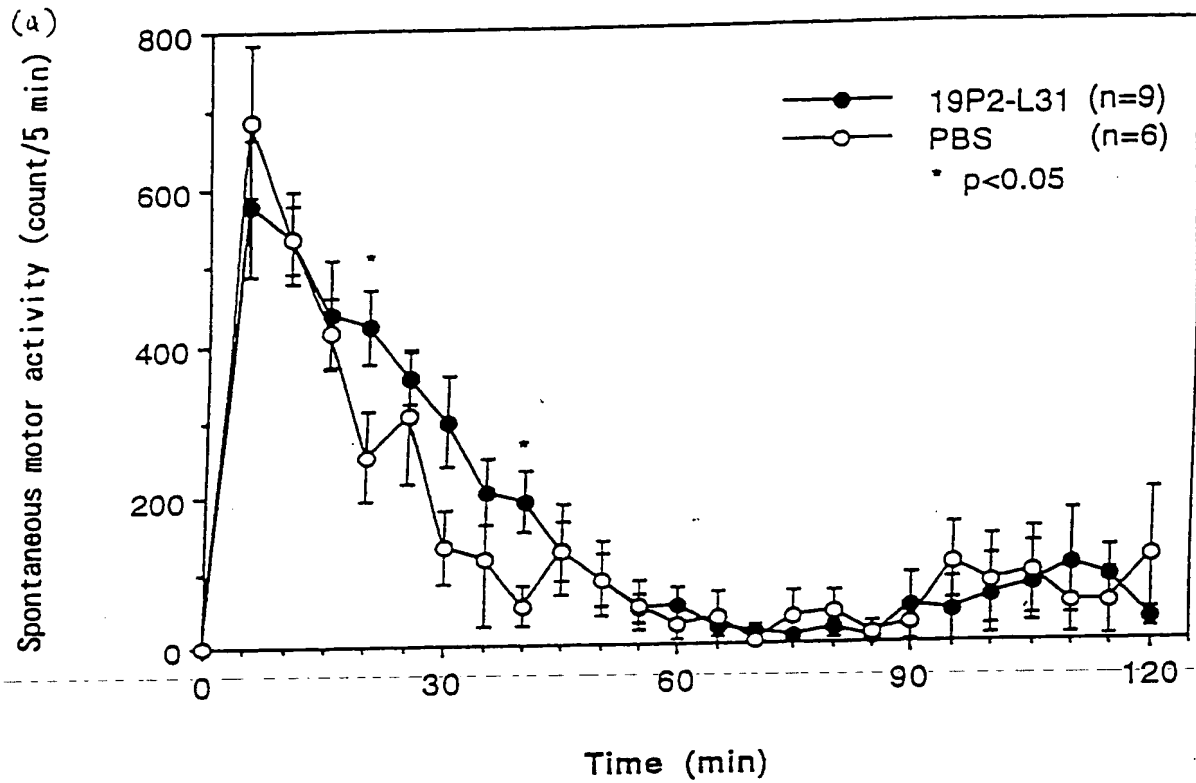
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Fig. 43



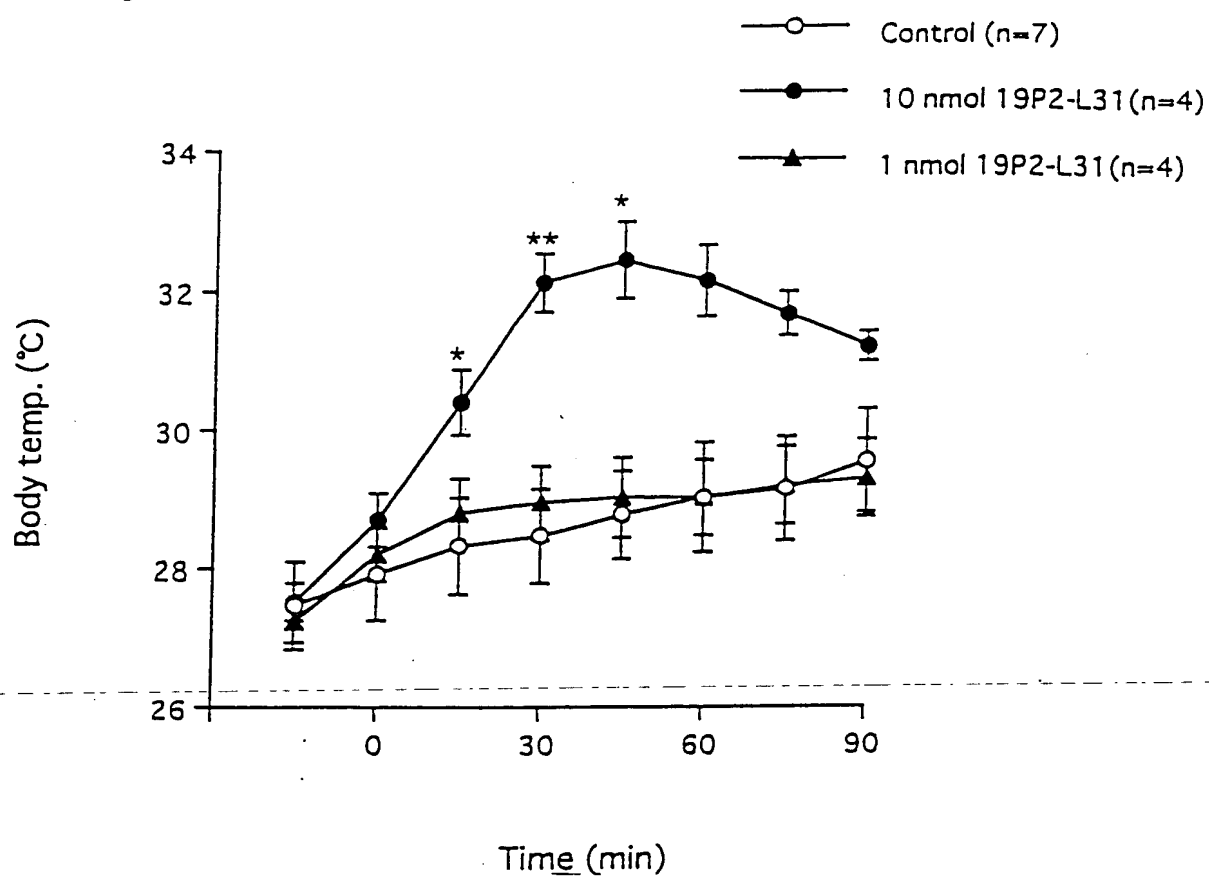
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Fig. 44



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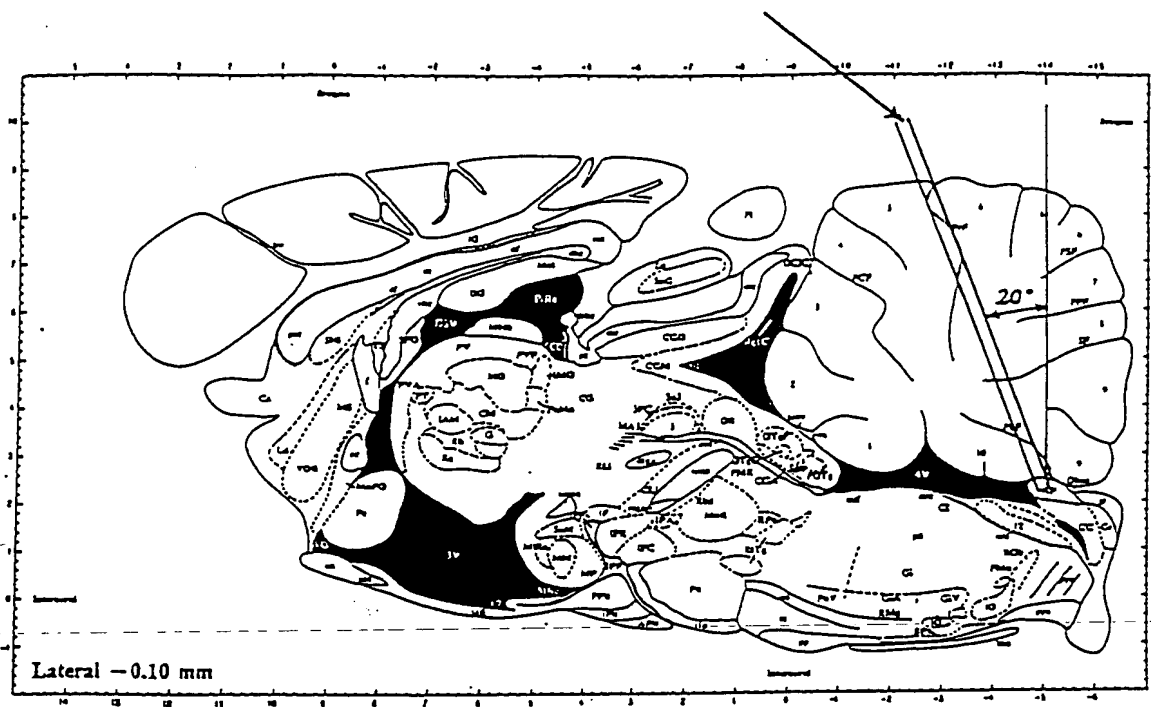
Fig. 45



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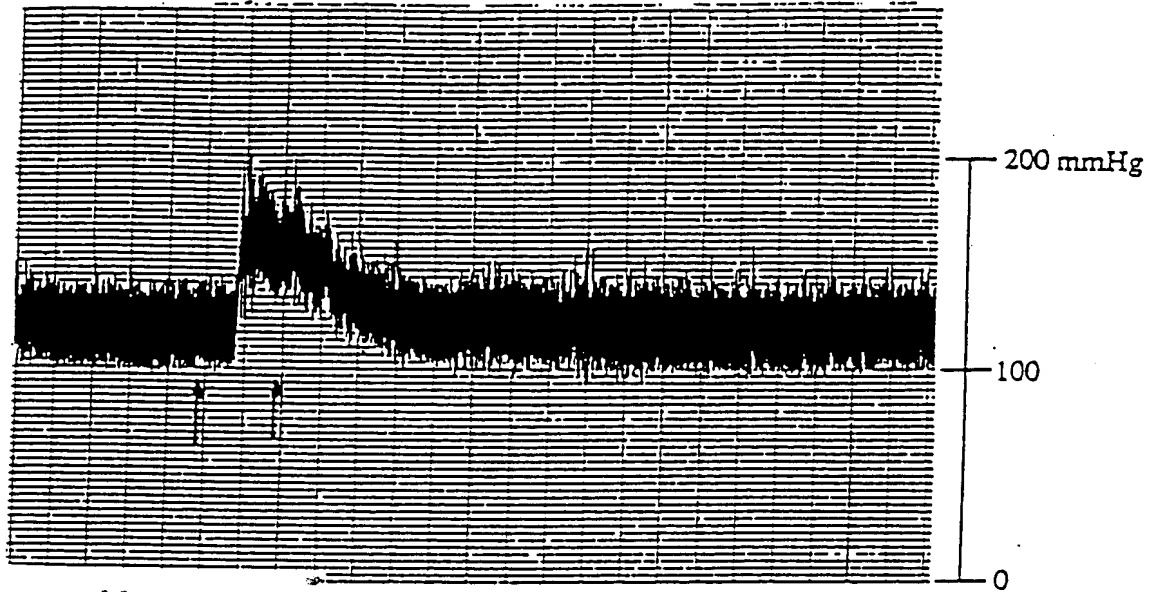
Fig. 46

Microinjection cannula

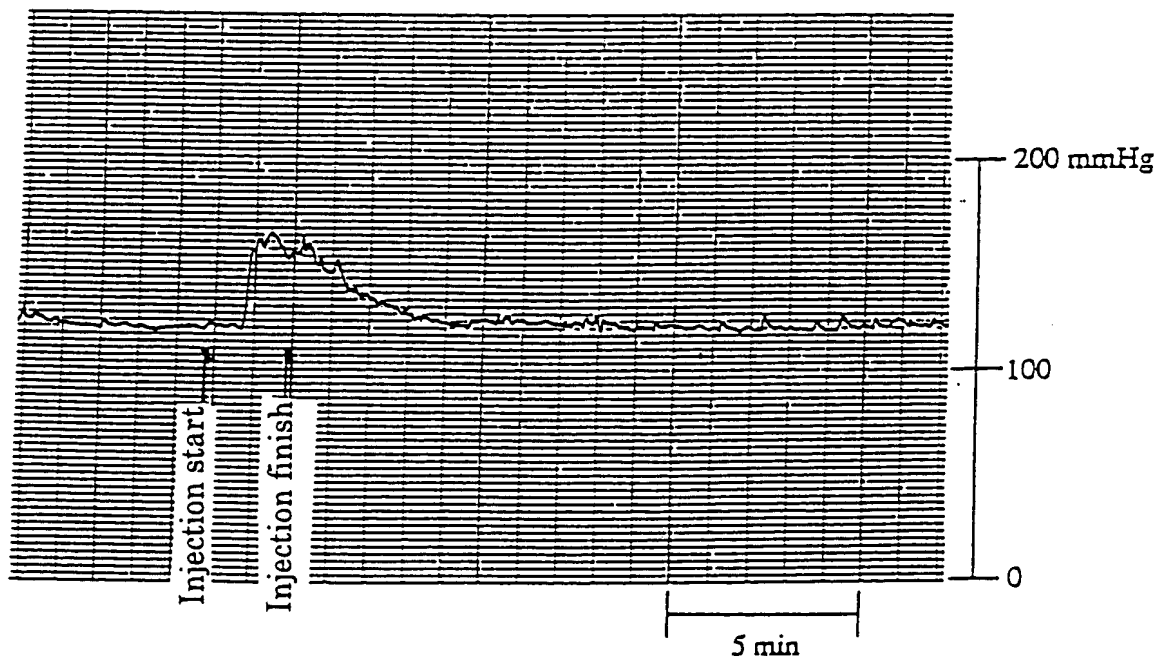


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Fig. 47
Pulse wave

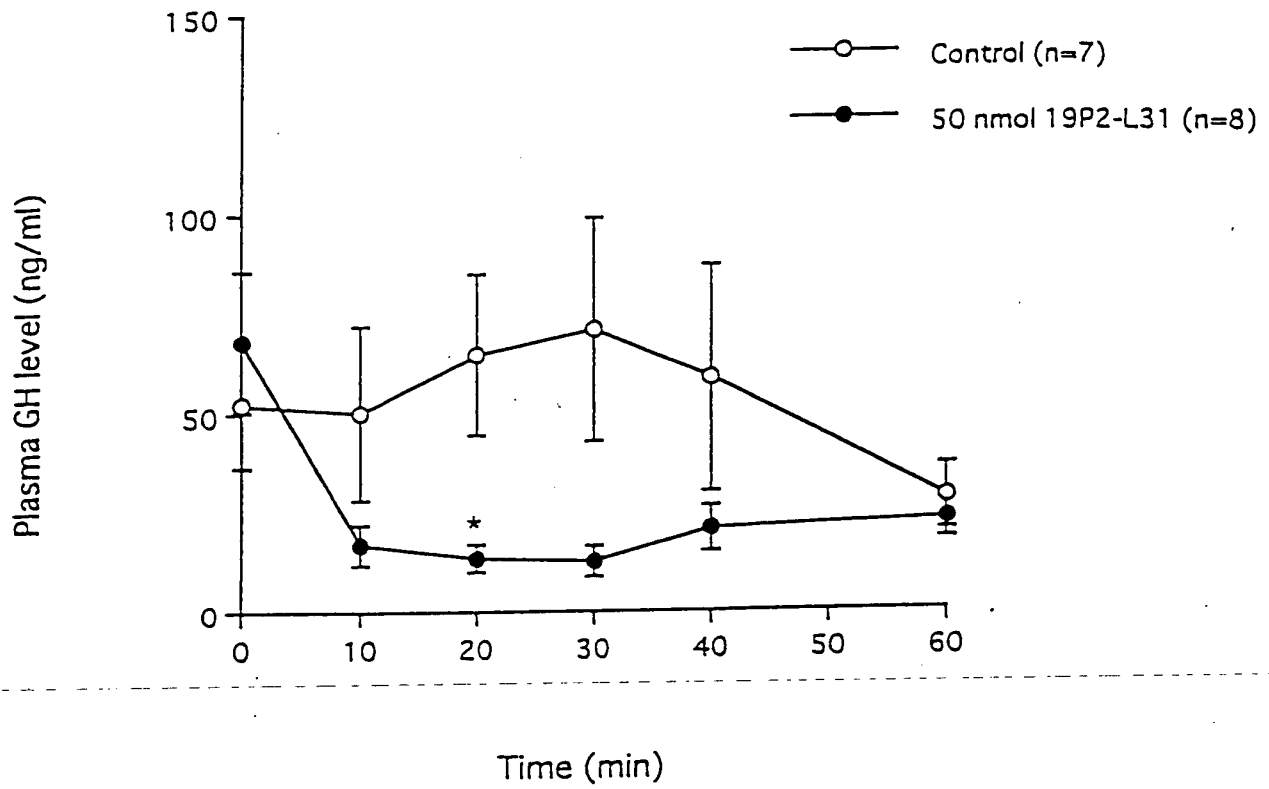


Average blood pressure



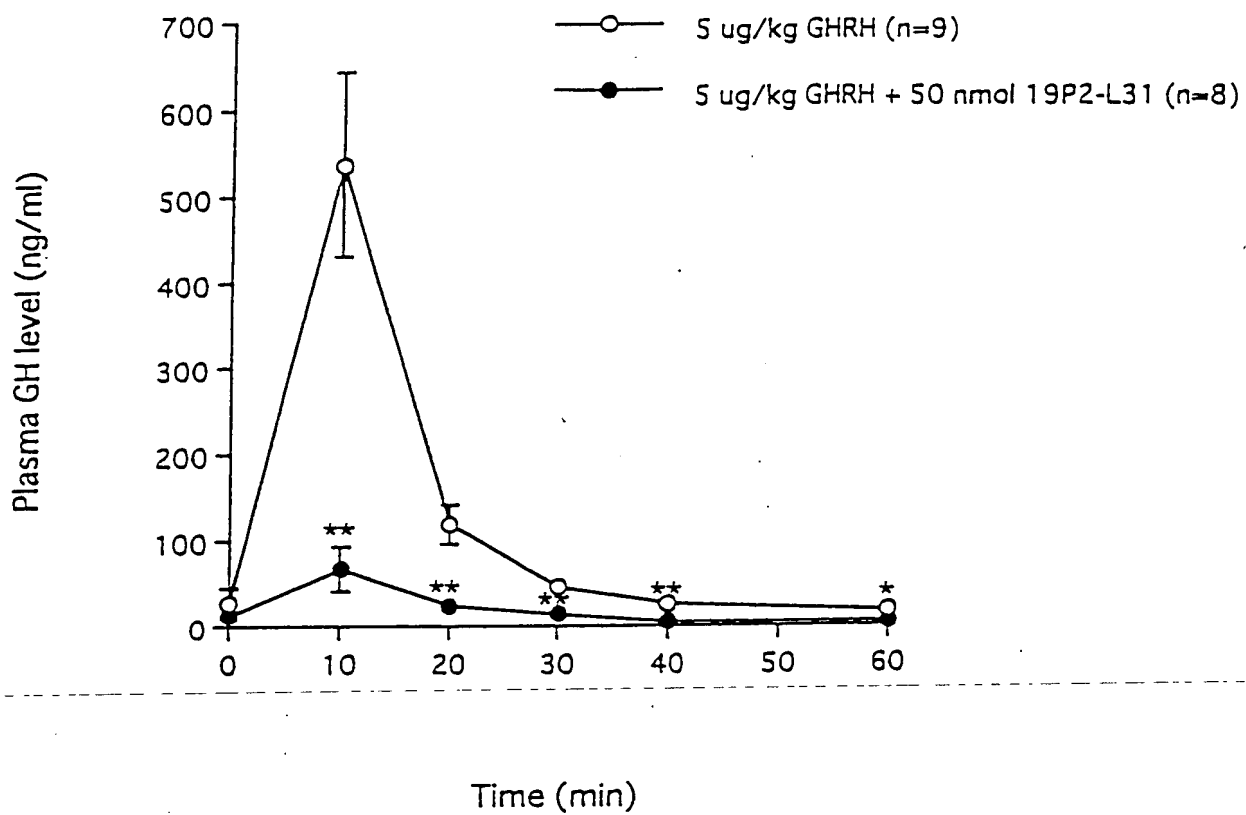
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Fig. 48



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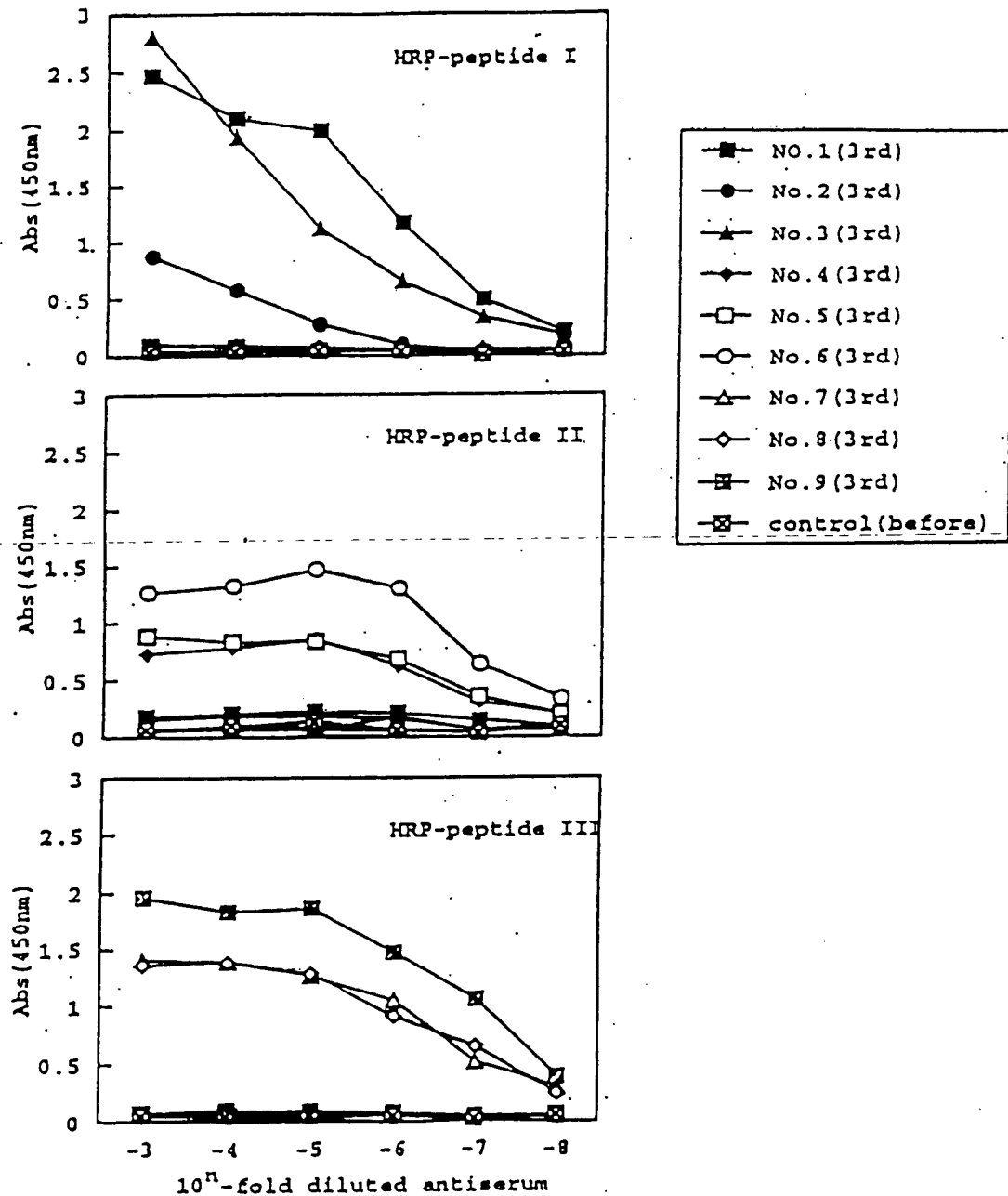
Fig. 49



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Fig. 50

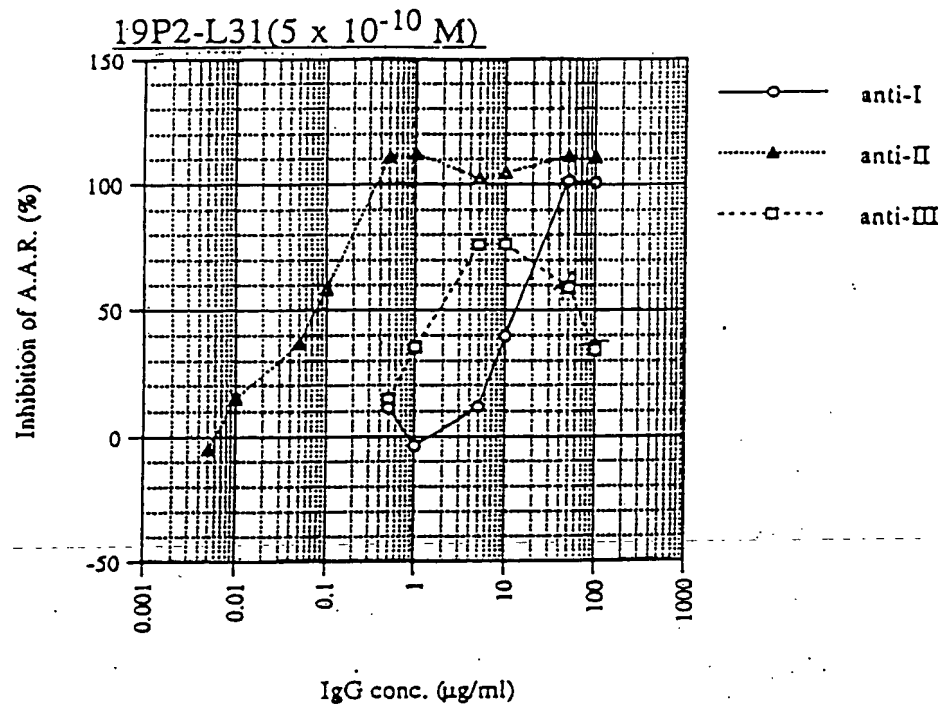
Titration curve of anti-bovine 19P2 peptide I, II
III serum using HRP-peptide I, II or III



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Fig. 51

Inhibition of A.A release by anti 19P2 peptide



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Fig. 52

5' ATG ACC TCA CTG CCC CCT CGA ACC ACT GCG GAC CCC GAT TTG TTT TCT GCG CCC 34
 Met Thr Ser Leu Pro Pro Gly Thr Thr Gly Asp Pro Asp Leu Phe Ser Gly Pro
 TCG CCA GCG GCG TCC ACT CCA GCG AAC CAG AOT CCA GAG OCT TCA CAG AOC AAT 108
 Ser Pro Ala Gly Ser Thr Pro Ala Asn Gln Ser Ala Glu Ala Ser Glu Ser Asn
 GTG TCT GCG ACC GTT CCC AGA OCT GCA CCA GTC ACC CCG TTC CAG ACC CTG CAA 162
 Val Ser Ala Thr Val Pro Arg Ala Ala Ala Val Thr Pro Phe Gln Ser Leu Gln
 CTA GTG CAG CAG CTG AAG CGA CTG ATC GTG ATG CTG TAC ACC ATC GTG GTC GTC 216
 Leu Val His Gln Leu Lys Gly Leu Ile Val Met Leu Tyr Ser Ile Val Val Val
 GTG GGT CTG GTG GCG AAC TCC CTT CTT GTG CTG GTG ATC CCG CCG GTG CCG CCG 270
 Val Gly Leu Val Gly Asn Cys Leu Leu Val Leu Val Ile Ala Arg Val Arg Arg
 CTG CAC AAC GTG ACC AAC TTC CTC ATC GCG AAC CTG CCG TTC TCC GAT GTG CTC 324
 Leu His Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu
 ATG TGT GCG GCG TGT GTC OCT CTC ACC CTG GCG TAC GCG TTT GAA CCG GGT GCG 378
 Met Cys Ala Ala Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly
 TCG GTG TTC GGT CGA GCG CTG TCC CAC CTT GTT TTC TTC CTG CAG CCG GTC ACC 432
 Trp Val Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr
 GTC TAC GTA TCG GTG TTC ACA CTC ACC ACA ATC OCT GTG GAC CCG TAT GTG GTC 486
 Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr Val Val
 CTG GTG CAC CCG CTA GGT GCG GCG ATT TCA CTG AAG CTC ACC GCG TAC GGT GTG 540
 Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Lys Leu Ser Ala Tyr Ala Val
 CTG GCG ATC TCG GGT CTA TCT GCA GTG CTG GCG CTG CCG GCG GCG GTG CAC ACC 594
 Leu Gly Ile Trp Ala Leu Ser Ala Val Leu Ala Leu Pro Ala Ala Val His Thr
 TAC CAT GTA GAG CTC AAG CCG CAC GAC GTG CCG CTC TCC GAG CAG TTC TCG GGT 648
 Tyr His Val Glu Leu Lys Pro His Asp Val Arg Leu Cys Glu Glu Phe Trp Gly
 TCG CAG CAG CCG CAG CGA CAG ATC TAT GCG TCG GCG CTG CTG CTG CCG ACC TAT 702
 Ser Gln Glu Arg Gln Arg Gln Ile Tyr Ala Trp Gly Leu Leu Leu Gly Thr Tyr
 TTG CTC GCG CTG CTG GCG ATT CTC CTG TCT TAC GTC CCG GTG TCG GTG AAG TTG 756
 Leu Leu Pro Leu Leu Ala Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu
 CCG AAC CCG GTG GTG OCT GCG ACC GTG ACC CAG ACC CAG OCT GAC TCG GAC CCA 810
 Arg Asn Arg Val Val Pro Gly Ser Val Thr Gln Ser Gln Ala Asp Trp Asp Arg
 GCG GGT CCG CCG CCG ACT TTC TCC CTG CTG GTG GTG GTG GTG GTG TTC GCG 864
 Ala Arg Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Phe Ala
 GTC TCC TCG CTG OCT CTG CAC ATT TTC AAC CTG CTG CCG GAC CTG GAC CCG GGT 918
 Val Cys Trp Leu Pro Leu His Ile Phe Asn Leu Leu Arg Asp Leu Asp Pro Arg
 GCG ATC GAC CCG TAC GCG TTC GCG CTG CAG CTC CTC TCC CAC TCG CTT GCG 972
 Ala Ile Asp Pro Tyr Ala Phe Gly Leu Val Gln Leu Leu Cys His Trp Leu Ala
 ATG ACC TCC GCG TCC TAC AAC CCG TTC ATC TAT GCG TCG CTG CAC GAC ACC TTC 1026
 Met Ser Ser Ala Cys Tyr Asn Pro Phe Ile Tyr Ala Trp Leu His Asp Ser Phe
 CGA GAG CAG CTA CCG AAG ATG CTT CTG TCT TCG CCG CCG AAG ATC GTG CTT CAT 1080
 Arg Glu Glu Leu Arg Lys Met Leu Leu Ser Trp Pro Arg Lys Ile Val Pro His
 GCG CAG AAT ATG ACC GTC AOT GTG GTC ATC TCA TCA 3'
 Gly Gln Asn Met Thr Val Ser Val Val Ile ...

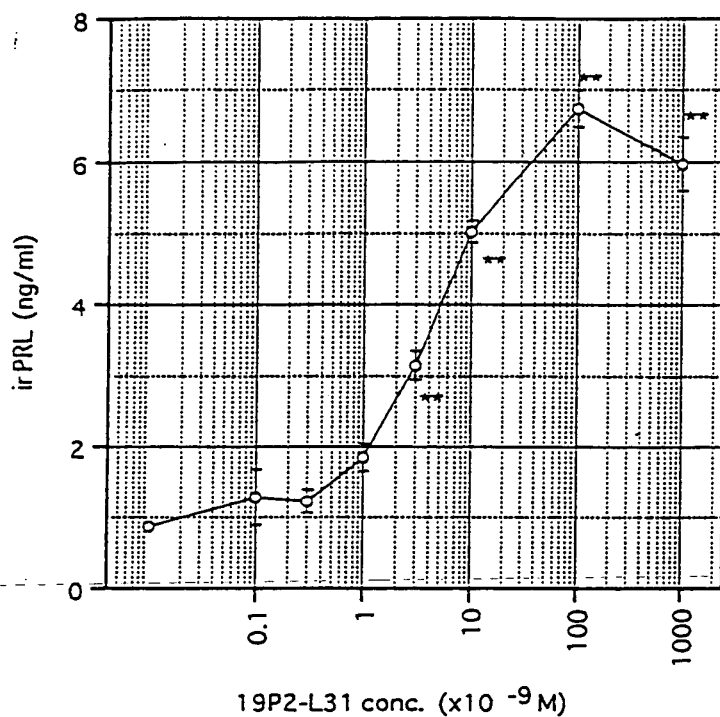
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70	80	90	100	110	120
TGCTGCTAGG	CTTAGTCCTC	CCAGGAGCTT	CCAGCCGAGC	CCACCAGCAC	TCCATGGAGA
130	140	150	160	170	180
CCCGCAGTGA	GTGCCTGGCA	TATGGAGGAC	AGCCACTGTC	ACCTCCCATC	CATATGCTTC
190	200	210	220	230	240
CCAAATGCCT	TGAGTACCCA	GCCCCTGAAT	GGGAGGTTAG	CCATCTCCTA	AGCCAGTGGT
250	260	270	280	290	300
TTCCAACCTT	CCTAATACAG	AACTTTTAAAT	ACAGATCCTT	ATGTTGTGGT	GACCCCCAGC
310	320	330	340	350	360
CAGAAAATTA	TTGTGATGCT	GTTTTTCATAG	TTGTAAGTTT	TGCTACTGTT	ATGGATCATA
370	380	390	400	410	420
ATGTTAATAT	CTGAAATGCA	GGATGTCCTGA	TATGCGCCCT	TCCCCC AAA	CAAAGGGAC
430	440	450	460	470	480
ACAACCCACA	GGTTGAGAGC	CTCTGGGATC	TAAGCAAAG	CTACCTTACC	ATGCAGTCAG
490	500	510	520	530	540
TTGGGAGATT	GGTCCTGTTA	AGATCTCCCC	AGAATGGTCC	TGTTTCCTGT	CCTCATCATT
550	560	570	580	590	600
CCCCTAACCC	ATCTTTGTGG	GGTCCCTTAA	GACTTTGGAG	GATGACAGTC	AGACAGGAAG
610	620	630	640	650	660
AGAATACTGA	TCCTGGCATA	TGTCTAAATA	AATTCCCTAA	AGCCACACCA	CTGCCCAGAT
670	680	690	700	710	720
ATGCCCAGCC	AGTGTAATCA	GGGTGGGTGC	CAACATGGCC	TGGTGCCCG	GTTTCCATCA
730	740	750	760	770	780
GCTTAGGGGC	TCCCGTGTCC	CATACGCTGC	TCTGACTCTT	TCCTTTCCAG	CCCCTGACAT
790	800	810	820	830	840
CAATCCTGCC	TGGTACACGG	GTCGTGGGAT	CAGGCCTGTG	GGCCGCTTCG	GGAGGAGGAG
850	860	870	880	890	900
GGCAGCCCTG	AGGGATGTCA	CCGGACCTGG	CCTGCGGTGC	CGGCTAAGCT	GCTTCCCACT
910	920	930	940	950	960
GGATGGAAGT	GCCAAGTTCT	CTCAGAGCTC	GAGAAGACAG	TGCTGCTGAG	TCGAC

[illegible]

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Fig. 55

PRL RIA RC-4B/C P19
Dose-Response for 30 min



Cell Culture: RC-4B/C P19

1×10^5 /well, for 2 Days
(12 well-plates)
(control: n=2, other points: n=4)

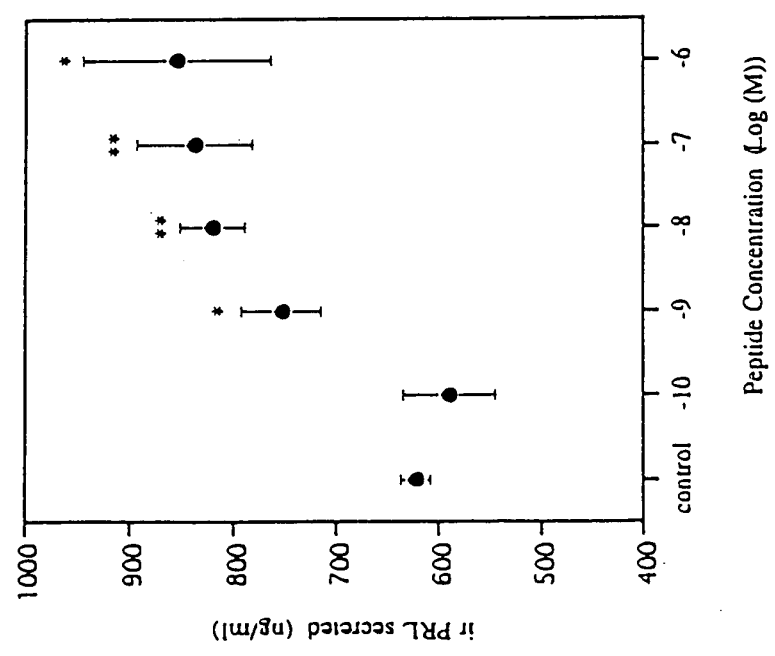
Wash 3 times
Pre-Incubation (for 15 min)
Wash twice, Add Samples
Incubation (for 30 min)
Sup. Collected, Centrifuged

Assay: Rat [125 I] Prolactin
Assay System (RIA) (Amersham)

**: $p < 0.01$ (students' t-test)

Fig. 56

Effect of bovine 19P2-L31 Peptides
on PRL Secretion from Pituitary Cells



Cell Culture: Rat Anterior Pituitary
Primary Culture
(from F344/N Female Lactating)
5.0x10⁵ /well,
for 4 Days (n=4)
(Poly-D-Lys. coated 24 well-plates)

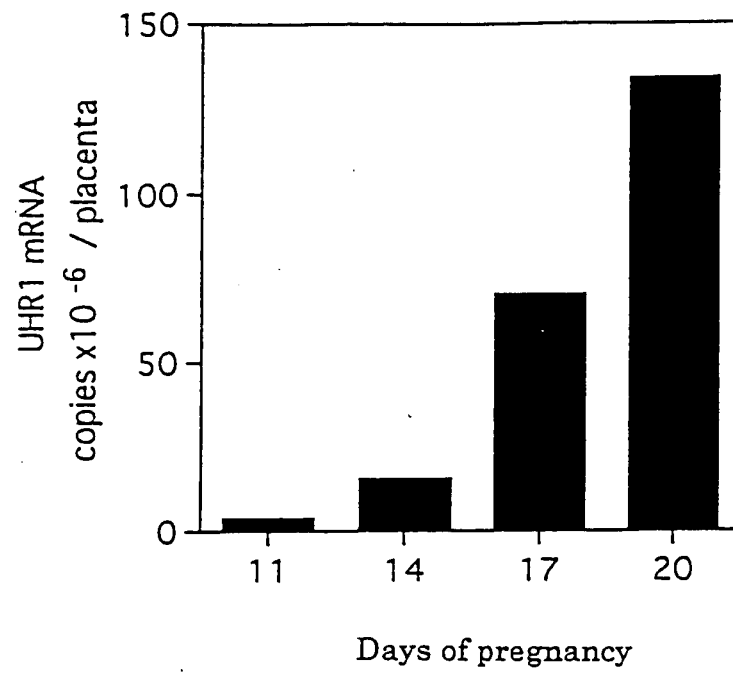
Wash 3 times
Pre-Incubation (for 1 hr)
Wash twice, Add Samples
Incubation (for 1 hr)
Sup. Collected, Centrifuged

Assay: Rat [125I] Prolactin
Assay System (RIA) (Amersham)

** : p<0.01 (students' t-test, compared to control)
* : p<0.05 (students' t-test, compared to control)

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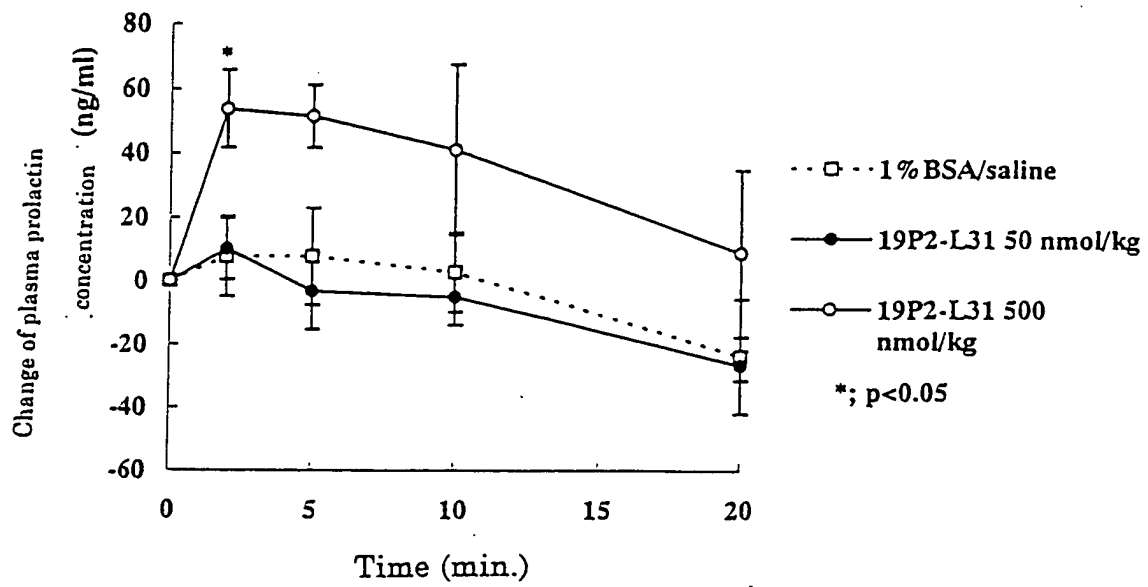
Fig. 57



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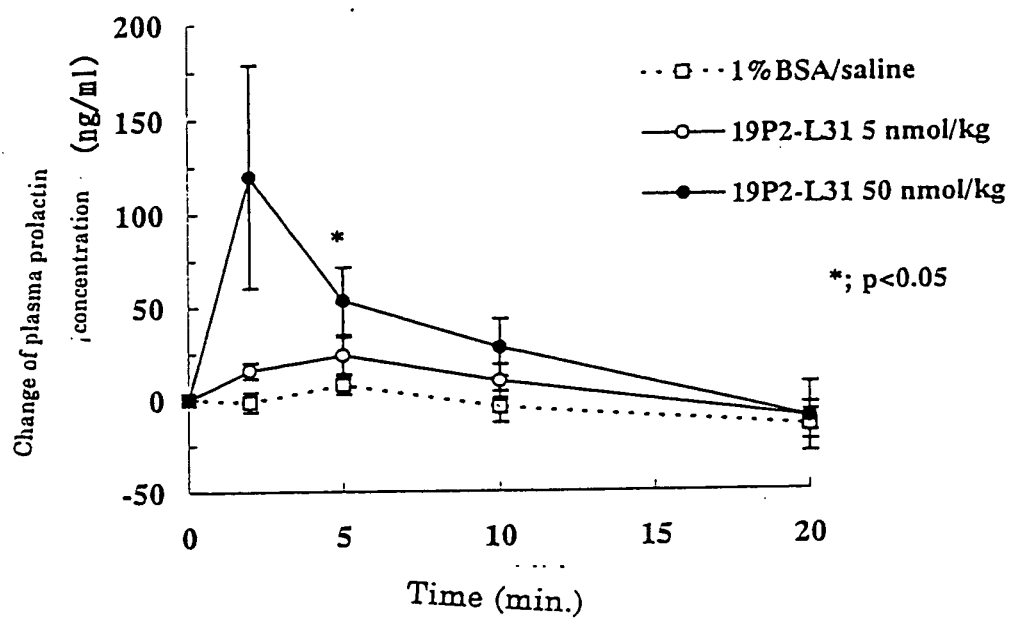
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Fig. 58



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Fig. 59



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Fig. 60

